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# OM protein - protein search, using sw model

Run on: August 10, 2005, 07:16:57 ; Search time 118,905 Seconds  
(without alignments)  
325.267 Million cell updates/sec

Title: US-09-743-818A-4\_COPY\_1\_100  
Perfect score: 524  
Sequence: 1 SMGVPALPGVPGVGFYF.....AAKAGAGLGVPVGLGVS 100

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	524	100.0	733	2	AAR56653
2	524	100.0	733	2	AAY01301
3	515	98.3	515	3	AAY69135
4	515	98.3	571	3	AAY69071
5	515	98.3	692	7	ADE40134
6	515	98.3	698	2	AAY01302
7	515	98.3	698	3	AAY69069
8	515	98.3	711	7	ADE40132
9	515	98.3	712	3	AAB08630
10	515	98.3	730	2	AAW46315
11	515	98.3	730	3	AAB08631
12	515	98.3	730	5	AAO17360
13	515	98.3	730	8	ADQ19747
14	515	98.3	731	3	AAY69068
15	515	98.3	731	4	AAB66657
16	515	98.3	731	6	ABU08725
17	515	98.3	731	7	ADL96420
18	515	98.3	731	7	ABG75223
19	515	98.3	757	7	ADP65160
20	448	85.5	559	8	ADQ66215
21	448	85.5	617	8	ADQ64761
22	375.5	71.7	472	4	AAB88422
23	351	67.0	870	4	ADQ65871
24	347	66.2	870	7	ADQ65827
25	334.5	63.8	663	7	ADM03792

26	326.5	62.3	864	7	ADP56670	Adp56670 Rat Prote
27	267.5	51.0	660	2	AAY01303	Aay01303 Human tro
28	201.5	38.5	91	5	AAY91258	Aay91258 Nucleic a
29	177.5	33.9	479	2	AAW49739	Aaw49739 Protein p
30	174	33.2	832	2	AAR80252	Aar80252 Polymer S
31	174	33.2	832	5	ABP53473	Abp53473 Protein p
32	174	33.2	936	2	AAW09221	Aaw09221 SELPORK-CS
33	174	33.2	936	3	AAV51891	Aav51891 Plasmid p
34	174	33.2	936	5	ABG31421	Abg31421 SELPORK-CS
35	174	33.2	936	7	ABW01637	Abw01637 Plasmid p
36	174	33.2	937	2	AAW53547	Aaw53547 Amino aci
37	173	33.0	312	5	ABP53480	Abp53480 Protein p
38	173	33.0	378	2	AAW09219	Aaw09219 SELPORK po
39	173	33.0	378	2	AAW53545	Aaw53545 Amino aci
40	173	33.0	378	5	AAV51889	Aav51889 Plasmid p
41	173	33.0	378	5	ABG31419	Abg31419 SELPORK pr
42	173	33.0	378	7	ABW01635	Abw01635 Plasmid p
43	173	33.0	936	2	AAR80251	Aar80251 Polymer S
44	173	33.0	936	5	ABP53472	Abp53472 Protein p
45	173	33.0	1002	2	AAW09218	Aaw09218 SELPORK po

## ALIGNMENTS

RESULT 1  
ID AAR56653 standard; protein; 733 AA.  
XX  
AC AAR56653;  
XX  
DT 25-MAR-2003 (revised)  
DT 22-MAR-1995 (first entry)  
XX  
DE Synthetic human tropoelastin (SHEL).  
XX  
KM Tropoelastin; pharmaceutical; surgical dressing.  
XX  
OS Synthetic.  
XX  
PN WO9414958-A1.  
XX  
PD 07-JUL-1994.  
XX  
PF 16-DEC-1993; 93MO-AU000655.  
XX  
PR 22-DEC-1992; 92AU-00006520.  
PR 28-JUN-1993; 93AU-00009661.  
XX  
PA (UNSY ) UNIV SYDNEY.  
XX  
PI Weiss AS, Martin SL;  
XX WPI: 1994-263633/32.  
DR N-PSDB; AAQ70941.  
XX  
PT Synthetic polynucleotide(s) - encode recombinant tropoelastins and  
PT variants.  
XX  
PS Disclosure; Page 30; 77pp; English.  
XX  
CC Human synthetic tropoelastin is susceptible to hydrolytic breakdown of  
CC the crosslinks. Such material may be useful in e.g. surgical  
CC applications, where the gradual loss of material over time is intended.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 733 AA;  
Query Match 100.0%; Score 524; DB 2; Length 733;  
Best Local Similarity 100.0%; Pred. No. 7.1e-36;  
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 SMGVPALPGVPGVGFYFAGAGLGGALPGCKLKPVPGLAGAGLGAFA 60

Db 1 SMGGVPGALPGGVPGGVFPYFGAGLGGALGPGGKPLKPVPGGLAGAGLGAFFPA 60  
 QY 61 VTFFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100  
 Db 61 VTFFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100

## RESULT 2

AAV01301  
 ID AAY01301 standard; protein; 733 AA.

AC AAY01301;

DT 07-JUN-1999 (first entry)

XX Amino acid sequence of synthetic human tropoelastin SHEL.

XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;  
 KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;  
 KM hand lotion; surgical implant; industrial product; human; SHEL.

XX Synthetic.

OS Homo sapiens.

XX MO9903886-A1.

XX 28-JAN-1999.

XX 17-JUL-1998; 98WO-AU000564.

XX 18-JUL-1997; 97AU-00008117.

XX (UNSY ) UNIV SYDNEY.

XX Weiss AS;

XX MPI; 1999-132162/11.

DR N-PSDB; AAX27704.

XX New derivatives of human tropoelastin - with elastin-like or  
 PT macromolecular binding properties, useful e.g. as surgical implants.

XX Disclosure; Fig 1; 82pp; English.

XX The invention relates to a derivative or variant of human tropoelastin  
 CC (hTE) having elastin-like and/or macromolecule (specifically  
 CC glycosaminoglycan (GAG)-binding properties. Cells containing vectors  
 CC comprising the nucleic acids encoding the variants or derivatives are  
 CC used to produce the proteins recombinantly. The tropoelastin derivatives  
 CC or hybrid proteins containing the derivatives are useful in medical,  
 CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
 CC wrinkle or hand lotions, also as surgical implants, foods and industrial  
 CC products. The hybrid protein have controllable GAG-binding properties,  
 CC depending on presence or absence of a specific fragment, designated  
 CC peptide 26a, from hTE. The present sequence represents the amino acid  
 CC sequence of the synthetic human tropoelastin SHEL

XX Sequence 733 AA;

Query Match 100.0%; Score 524; DB 2; Length 733;

Best Local Similarity 100.0%; Pred. No. 7.1e-36;

Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SMGGVPGALPGGVPGGVFPYFGAGLGGALGPGGKPLKPVPGGLAGAGLGAFFPA 60

Db 1 SMGGVPGALPGGVPGGVFPYFGAGLGGALGPGGKPLKPVPGGLAGAGLGAFFPA 60

QY 61 VTFFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100

Db 61 VTFFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100

RESULT 3  
 ID AAY69135  
 AA69135 standard; protein; 515 AA.

XX AAY69135;

DT 30-MAY-2000 (first entry)

XX Amino acid sequence of a human tropoelastin derivative.

XX Tropoelastin; derivative; proteolysis; protease; antiwrinkle;  
 KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;  
 KM peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.

XX Homo sapiens.

XX WO200004043-A1.

XX 27-JAN-2000.

XX 19-JUL-1999; 99WO-AU000580.

XX 17-JUL-1998; 98AU-00004723.

XX (UNSY ) UNIV SYDNEY.

XX Weiss AS;

XX MPI; 2000-182399/16.

XX New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and  
 PT cell growth.

XX Disclosure; Page 131-133; 136pp; English.

XX The present sequence represents a human tropoelastin derivative, which is  
 CC representative of tropoelastin derivatives of the invention. In the  
 CC tropoelastin derivatives of the invention a subsequence has been mutated  
 CC so that susceptibility to proteolysis is reduced or eliminated, or a  
 CC subsequence has been inserted so that susceptibility to proteolysis is  
 CC increased. The derivatives have with reduced susceptibility, and can be  
 CC used where the wild-type protein would be degraded too easily, e.g. in  
 CC contact with serum or wound exudate. The tropoelastin derivatives provide  
 CC competitive inhibition of protease activity. The tropoelastin  
 CC derivatives, and other polypeptides containing tropoelastin derivative-  
 CC derived protease-susceptibility sites, are useful in human or veterinary  
 CC medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents  
 CC and for inducing chemotaxis. They are also useful for proliferation or  
 CC growth inhibition, particularly of smooth muscle cells, epithelial or  
 CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.  
 CC Peptidomimetics that mimic the protease cleavage site in tropoelastin  
 CC derivatives are competitive inhibitors of the protease, and are used for  
 CC protecting against lung damage caused by elastin, for inhibiting or  
 CC controlling localized growth of cancers or metastases, or to limit  
 CC protease activity that causes blood clotting

XX Sequence 515 AA;

Query Match 98.3%; Score 515; DB 3; Length 515;

Best Local Similarity 100.0%; Pred. No. 2.9e-35;

Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPGALPGGVPGGVFPYFGAGLGGALGPGGKPLKPVPGGLAGAGLGAFFPAVT 62

Db 1 GGVPGALPGGVPGGVFPYFGAGLGGALGPGGKPLKPVPGGLAGAGLGAFFPAVT 60

QY 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100

Db 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 98

## RESULT 4

AA69071

ID AAY69071 standard; protein; 571 AA.  
 XX  
 AC AAY69071;  
 XX  
 DT 30-MAY-2000 (first entry)  
 XX  
 DE Amino acid sequence of a human tropoelastin derivative.  
 XX  
 KW Tropoelastin; derivative; proteolysis; protease; antiwrinkle;  
 KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;  
 KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200004043-A1.  
 XX  
 PD 27-JAN-2000.  
 XX  
 PF 19-JUL-1999; 99MO-AU0000580.  
 XX  
 PR 17-JUL-1998; 98AU-00004723.  
 XX  
 PA (UNSY ) UNIV SYDNEY.  
 XX  
 PI Weiss AS;  
 XX  
 DR MPI; 2000-182399/16.  
 XX  
 PT New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and  
 PT cell growth.  
 XX  
 PS Disclosure; Page 115-117; 136pp; English.  
 XX  
 CC The present sequence represents a human tropoelastin derivative, which is  
 CC representative of tropoelastin derivatives of the invention. In the  
 CC tropoelastin derivatives of the invention a subsequence has been mutated  
 CC so that susceptibility to proteolysis is reduced or eliminated, or a  
 CC subsequence has been inserted so that susceptibility to proteolysis is  
 CC increased. The derivatives have with reduced susceptibility, and can be  
 CC used where the wild-type protein would be degraded too easily, e.g. in  
 CC contact with serum or wound exudate. The tropoelastin derivatives provide  
 CC competitive inhibition of protease activity. The tropoelastin  
 CC derivatives, and other polypeptides containing tropoelastin derivative-  
 CC derived protease-susceptibility sites, are useful in human or veterinary  
 CC medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents  
 CC and for inducing chemotaxis. They are also useful for proliferation or  
 CC growth inhibition, particularly of smooth muscle cells, epithelial or  
 CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.  
 CC Peptidomimetics that mimic the protease cleavage site in tropoelastin  
 CC derivatives are competitive inhibitors of the protease, and are used for  
 CC protecting against lung damage caused by elastin, for inhibiting or  
 CC controlling localized growth of cancers or metastases, or to limit  
 CC protease activity that causes blood clotting  
 XX  
 SQ Sequence 571 AA:  
 Query Match 98.3%; Score 515; DB 3; length 571;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-35;  
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GGVPGALPGVPGVFPFGAGLALGGGALGPGKPLKPPVGLAGLGLGAFPAVT 62  
 DB 1 GGVPGALPGVPGVFPFGAGLALGGGALGPGKPLKPPVGLAGLGLGAFPAVT 60  
 QY 63 FPGALVPGVADAAAAYKAAKAGAGLGVPGVGLIGVS 100  
 DB 61 FPGALVPGVADAAAAYKAAKAGAGLGVPGVGLIGVS 98

AC ADE40134;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human NOV16b protein - SEQ ID 40.  
 XX  
 KW NOVX; cardiant; antiarteriosclerotic; hypotensive; cyostatic; anorectic;  
 KW antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;  
 KW antiparkinsonian; antiaesthetic; gynaecological; cardiomyopathy;  
 KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;  
 KW multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;  
 KW asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;  
 KW tissue typing; human; NOV.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003064589-A2.  
 XX  
 PD 07-AUG-2003.  
 XX  
 PF 02-AUG-2002; 2002MO-US024483.  
 XX  
 PR 02-AUG-2001; 2001US-0309501P.  
 PR 03-AUG-2001; 2001US-0310291P.  
 PR 07-AUG-2001; 2001US-0310544P.  
 PR 08-AUG-2001; 2001US-0310951P.  
 PR 09-AUG-2001; 2001US-0311292P.  
 PR 13-AUG-2001; 2001US-0311979P.  
 PR 16-AUG-2001; 2001US-0312892P.  
 PR 17-AUG-2001; 2001US-0313201P.  
 PR 17-AUG-2001; 2001US-0313415P.  
 PR 20-AUG-2001; 2001US-0313643P.  
 PR 20-AUG-2001; 2001US-0313702P.  
 PR 21-AUG-2001; 2001US-0314031P.  
 PR 23-AUG-2001; 2001US-0314466P.  
 PR 28-AUG-2001; 2001US-0315403P.  
 PR 29-AUG-2001; 2001US-0315853P.  
 PR 17-SEP-2001; 2001US-0322716P.  
 PR 21-SEP-2001; 2001US-0323994P.  
 PR 14-DEC-2001; 2001US-0340233P.  
 PR 05-FEB-2002; 2002US-0354591P.  
 PR 19-MAR-2002; 2002US-0365478P.  
 PR 19-APR-2002; 2002US-0373814P.  
 PR 19-APR-2002; 2002US-0373825P.  
 PR 19-APR-2002; 2002US-0373989P.  
 PR 23-APR-2002; 2002US-0374632P.  
 PR 07-JUN-2002; 2002US-0386971P.  
 PR 01-AUG-2002; 2002US-00210172.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 PA  
 PI Kekuda R, Miller CE, Paturajan M, Pena CE, Rieger DK;  
 PI Shumkets RA, Zerhusen BD, Li L, Ji W, Padigan M, Casman SJ;  
 PI Voss EZ, Boldo FL, Gorman L, Leite MW, Vernet CM, Anderson DW;  
 PI Guo X, Zhong M, Gerlach VL, Hjalte T, Rastelli L, Spletz KA;  
 PI Edinger SR, Ellerman K, Malyanar UM, Machedugali JR, Stone DJ;  
 PI Alsobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;  
 PI Sultheon G;  
 XX  
 DR MPI; 2003-663472/62.  
 DR N-PSDB; ADE40133.  
 XX  
 PT New NOVX polypeptides and nucleic acids, useful for preventing or  
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
 PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or  
 PT pharmacogenomics.  
 XX  
 PS Claim 1; SEQ ID NO 40; 560pp; English.  
 XX  
 CC The invention relates to a novel NOVX polypeptide. The polypeptide of the  
 CC invention demonstrates cardiant, antiarteriosclerotic, hypotensive,  
 CC cyostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,  
 CC neuroprotective, nootropic, antiparkinsonian, antiaesthetic and

CC gynaeological activities and may be useful in diagnosing, treating or  
 CC preventing NOXV-associated disorders including cardiomyopathy,  
 CC atherosclerosis, hypertension, cancer, obesity, diabetes AIDS, multiple  
 CC sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's  
 CC disease, asthma or fertility disorders. Furthermore, the polypeptides may  
 CC be utilised as vaccines whilst the nucleic acids may be used as  
 CC hybridisation probes, in gene therapy, chromosome mapping, tissue typing,  
 CC preventive medicine and pharmacogenomics. The current sequence is that of  
 CC the human NOV protein of the invention.

XX SQ Sequence 692 AA;

Query Match 98.3%; Score 515; DB 7; Length 692;

Best Local Similarity 100.0%; Pred. No. 3.8e-35;  
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPGAIPEGVPGVFFYPGAGLGGALGPGGKPLKVPVPGLAGAGLGAFPAYT 62  
 DB 27 GGVPGAIPEGVPGVFFYPGAGLGGALGPGGKPLKVPVPGLAGAGLGAFPAYT 86  
 QY 63 FPGALVPGGVADAAAYRAAKAGAGLGGVPGVGLGVS 100  
 DB 87 FPGALVPGGVADAAAYRAAKAGAGLGGVPGVGLGVS 124

RESULT 6

AAV01302 standard; protein; 698 AA.

XX AAV01302;

DT 07-JUN-1999 (first entry)

XX Human tropoelastin variant SHELDelta26A.

XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;  
 KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;  
 KW hand lotion; surgical implant; industrial product; human; SHELD; variant.

OS Homo sapiens.  
 OS Synthetic.

XX WO9303886-A1.

XX 28-JAN-1999.

XX PF 17-JUL-1998; 98WO-AU000564.

XX PR 18-JUL-1997; 97AU-00008117.

XX (UNSY ) UNIV SYDNEY.

XX PA Weiss AS;

XX PI

XX DR WPI; 1999-132162/11.

XX PT New derivatives of human tropoelastin - with elastin-like or  
 PT macromolecular binding properties, useful e.g. as surgical implants.

XX PS Claim 13; Fig 2; 82pp; English.

CC The invention relates to a derivative or variant of human tropoelastin  
 CC (hTE) having elastin-like and/or macromolecule (specifically  
 CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors  
 CC comprising the nucleic acids encoding the variants or derivatives are  
 CC used to produce the proteins recombinantly. The tropoelastin derivatives  
 CC or hybrid proteins containing the derivatives are useful in medical,  
 CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
 CC wrinkle or hand lotions, also as surgical implants, foods and industrial  
 CC products. The hybrid protein have controllable GAG-binding properties,  
 CC depending on presence or absence of a specific fragment, designated  
 CC peptide 26A, from hTE. The present sequence represents the synthetic  
 CC human tropoelastin variant SHELDelta26A

XX SQ Sequence 698 AA;

Query Match 98.3%; Score 515; DB 2; Length 698;

Best Local Similarity 100.0%; Pred. No. 3.9e-35;  
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPGAIPEGVPGVFFYPGAGLGGALGPGGKPLKVPVPGLAGAGLGAFPAYT 62  
 DB 1 GGVPGAIPEGVPGVFFYPGAGLGGALGPGGKPLKVPVPGLAGAGLGAFPAYT 60  
 QY 63 FPGALVPGGVADAAAYRAAKAGAGLGGVPGVGLGVS 100  
 DB 61 FPGALVPGGVADAAAYRAAKAGAGLGGVPGVGLGVS 98

RESULT 7

AAV69069 standard; protein; 698 AA.

XX AAV69069;

DT 30-MAY-2000 (first entry)

XX Amino acid sequence of a human reduced tropoelastin derivative.

XX Tropoelastin; derivative; SHELDelta-26A; SHELD; proteolysis; protease;  
 KW anti-wrinkle; hand lotion; bulking agent; chemotaxis; proliferation;  
 KW growth inhibition; peptidomimetic; lung damage; elastin; cancer;  
 KW metastasis; blood clotting.

OS Synthetic.

OS Homo sapiens.

XX WO200004043-A1.

XX 27-JAN-2000.

XX PF 19-JUL-1999; 99WO-AU000580.

XX PR 17-JUL-1998; 98AU-00004723.

XX (UNSY ) UNIV SYDNEY.

XX PA Weiss AS;

XX PI WPI; 2000-182399/16.

XX DR N-PSDB, AA261144.

XX PT New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and  
 PT cell growth.

XX PS Disclosure; Page 110-112; 136pp; English.

CC The present sequence represents a human reduced tropoelastin derivative,  
 CC designated SHELDelta-26A. The sequence is produced by removing exon 26a  
 CC of SHELD (SHELD not defined). The protein is representative of tropoelastin  
 CC derivatives of the invention, in which a subsequence has been mutated so  
 CC that susceptibility to proteolysis is reduced or eliminated, or a  
 CC subsequence has been inserted so that susceptibility to proteolysis is  
 CC increased. The derivatives have with reduced susceptibility, and can be  
 CC used where the wild-type protein would be degraded too easily, e.g. in  
 CC contact with serum or wound exudate. The tropoelastin derivatives provide  
 CC competitive inhibition of protease activity. The tropoelastin  
 CC derivatives, and other polypeptides containing tropoelastin derivative-  
 CC derived protease-susceptibility sites, are useful in human or veterinary  
 CC medicine, cosmetics (e.g. anti-wrinkle or hand lotions), as bulking agents  
 CC and for inducing chemotaxis. They are also useful for proliferation or  
 CC growth inhibition, particularly of smooth muscle cells, epithelial or  
 CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.  
 CC Peptidomimetics that mimic the protease cleavage site in tropoelastin  
 CC derivatives are competitive inhibitors of the protease, and are used for  
 CC protecting against lung damage caused by elastin, for inhibiting or

CC controlling localized growth of cancers or metastases, or to limit  
CC protease activity that causes blood clotting  
XX  
SQ Sequence 698 AA;

Query Match 98.3%; Score 515; DB 3; Length 698;  
Best Local Similarity 100.0%; Pred. No. 3.9e-35;  
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPGAIPGVPFGVFPAGLGGALGGALPGGKPLKVPVGGIAGAGLGAFAFPAVT 62  
DB 1 GGVPGAIPGVPFGVFPAGLGGALGGALPGGKPLKVPVGGIAGAGLGAFAFPAVT 60  
QY 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGIGVS 100  
DB 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGIGVS 98

RESULT 8  
ADE40132  
ID ADE40132 standard; protein; 711 AA.  
XX  
AC ADE40132;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human NOV16a protein - SEQ ID 38.

XX  
DE Human NOV16a protein - SEQ ID 38.  
XX  
NOVX: cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;  
KW antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;  
KW antiparkinsonian; antiaesthetic; gynaecological; cardiomyopathy;  
KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;  
KW multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;  
KW asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;  
KW tissue typing; human; NOV.

XX  
OS Homo sapiens.  
XX  
PN MO2003064589-A2.  
XX  
PD 07-AUG-2003.

PF 02-AUG-2002; 2002WO-US024483.

XX  
PR 02-AUG-2001; 2001US-0309501P.  
PR 03-AUG-2001; 2001US-0310291P.  
PR 07-AUG-2001; 2001US-0310544P.  
PR 08-AUG-2001; 2001US-0310951P.  
PR 09-AUG-2001; 2001US-0311292P.  
PR 13-AUG-2001; 2001US-0311979P.  
PR 16-AUG-2001; 2001US-0312892P.  
PR 17-AUG-2001; 2001US-0313201P.  
PR 17-AUG-2001; 2001US-0313415P.  
PR 20-AUG-2001; 2001US-0313643P.  
PR 20-AUG-2001; 2001US-0313702P.  
PR 21-AUG-2001; 2001US-0314031P.  
PR 23-AUG-2001; 2001US-0314466P.  
PR 26-AUG-2001; 2001US-0315403P.  
PR 29-AUG-2001; 2001US-0315853P.  
PR 17-SEP-2001; 2001US-0322716P.  
PR 21-SEP-2001; 2001US-0323994P.  
PR 14-DEC-2001; 2001US-0340233P.  
PR 05-FEB-2002; 2002US-0354591P.  
PR 19-MAR-2002; 2002US-0365478P.  
PR 19-APR-2002; 2002US-0373814P.  
PR 19-APR-2002; 2002US-0373825P.  
PR 19-APR-2002; 2002US-0373989P.  
PR 23-APR-2002; 2002US-0374632P.  
PR 07-JUN-2002; 2002US-0386971P.  
PR 01-AUG-2002; 2002US-00210172.

XX  
FA (CURA-) CURAGEN CORP.  
XX

PI Kekuda R, Miller CE, Patturajan M, Pena CE, Rieger DK;  
PI Shinkets RA, Zernhusen BD, Li L, Ji W, Padigar M, Casman SJ;  
PI Voss EZ, Boldog RU, Gorman L, Leite MW, Vernet CAM, Anderson DW;  
PI Guo X, Zhong M, Gerlach VL, Hjalt T, Raestelli L, Spytek KA;  
PI Edinger SR, Ellerman K, Malyankar UM, Macdonald JR, Stone DJ;  
PI Alsbrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;  
PI Smithson G;

DR WPI, 2003-663472/62.  
DR N-PSDB; ADE40131.

XX  
XX New NOVX polypeptides and nucleic acids, useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or  
PT pharmacogenomics.

PS Claim 1; SEQ ID NO 38; 560pp; English.

XX  
XX The invention relates to a novel NOVX polypeptide. The polypeptide of the  
CC invention demonstrates cardiant, antiarteriosclerotic, hypotensive,  
CC cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,  
CC neuroprotective, nootropic, antiparkinsonian, antiaesthetic and  
CC gynaecological activities and may be useful in diagnosing, treating or  
CC preventing NOVX-associated disorders including cardiomyopathy,  
CC atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple  
CC sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's  
CC disease, asthma or fertility disorders. Furthermore, the polypeptides may  
CC be utilised as vaccines whilst the nucleic acids may be used as  
CC hybridisation probes, in gene therapy, chromosome mapping, tissue typing,  
CC preventative medicine and pharmacogenomics. The current sequence is that of  
CC the human NOV protein of the invention.

XX  
SQ Sequence 711 AA;

Query Match 98.3%; Score 515; DB 7; Length 711;  
Best Local Similarity 100.0%; Pred. No. 3.9e-35;  
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPGAIPGVPFGVFPAGLGGALGGALPGGKPLKVPVGGIAGAGLGAFAFPAVT 62  
DB 27 GGVPGAIPGVPFGVFPAGLGGALGGALPGGKPLKVPVGGIAGAGLGAFAFPAVT 86

QY 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGIGVS 100  
DB 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGIGVS 124

RESULT 9

AA08630  
ID AA08630 standard; peptide; 712 AA.

XX  
AC AA08630;

XX  
DT 20-DEC-2000 (first entry)

XX  
DE Amino acid sequence of a human elastin polypeptide.

XX  
KW Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation;  
KW smooth muscle cell differentiation; smooth muscle cell migration;  
KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;  
KW vascular bypass graft stenosis; transplant arteriopathy; dissection;  
KW SVAS; hypertension; transplant arteriopathy.

XX  
OS Homo sapiens.

XX  
PN WO200050068-A2.

XX  
PD 31-AUG-2000.

XX  
PF 28-FEB-2000; 2000WO-US002526.

XX  
PR 26-FEB-1999; 99US-00258217.

XX



XX 26-FEB-1999; 99US-00258217.  
XX (UTAH ) UNIV UTAH RES FOUND.  
XX Keating MT, Li DY;  
XX WPI; 2000-533134/48.  
XX  
XX Elastin based compositions useful for treating atherosclerosis,  
XX PT restenosis, vascular bypass graft stenosis, transplant arteriopathy,  
XX PT aneurysm, dissection SVAS and/or hypertension.  
XX  
XX Example 3; Page 48; 79pp; English.  
XX  
XX The present sequence represents a fusion protein, comprising human  
XX CC elastin and c-myc, preceded by a His tag. The protein is used in  
XX CC compositions of the invention. The specification describes elastin based  
XX CC compositions that are potent regulators of smooth muscle cell  
XX CC proliferation, differentiation and migration in vivo. The elastin-based  
XX CC compositions comprise at least one elastic fibre, elastins, tropoelastins  
XX CC (or fragments of them) which have biological activities comprising:  
XX CC inhibiting the proliferation of smooth muscle cells in vivo; stimulating  
XX CC the differentiation of smooth muscle cell in vivo; and regulating the  
XX CC migration of smooth muscle cells in vivo. The compositions may be used  
XX CC for the prophylaxis or treatment of a disorder characterized by  
XX CC diminished capacity to regulate smooth muscle cell function such as  
XX CC atherosclerosis, restenosis, vascular bypass graft stenosis, transplant  
XX CC arteriopathy, aneurysm and/or dissection. Disorders which may be treated  
XX CC also include SVAS (undefined), hypertension, and transplant arteriopathy  
XX  
SQ Sequence 730 AA;

Query Match 98.3%; Score 515; DB 3; Length 730;  
Best Local Similarity 100.0%; Pred. No. 4e-35;  
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPGAI PGCVPGCVFPFGAGLGLAGLGGALGPGGKPLKVPVPGIAGAGLGAFAFPAVT 62  
DB 36 GGVPGAI PGCVPGCVFPFGAGLGLAGLGGALGPGGKPLKVPVPGIAGAGLGAFAFPAVT 95

QY 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100  
DB 96 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 133

## RESULT 12

AAO17360  
ID AAO17360 standard; protein; 730 AA.

AC AAO17360;  
DT 19-JUL-2002 (first entry)

XX Human elastin.

XX Human; endometriosis; DNA chip; fibronectin; p27; reticulocalbin;  
XX aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin;  
XX insulin-like growth factor binding protein-2; alpha-2 type IV collagen;  
XX transmembrane receptor PTK7; collagen type XVIII alpha 1;  
XX platelet derived growth factor receptor alpha; laminin M chain;  
XX subtilisin like protein PACE4; nidogen.

XX Homo sapiens.

XX EPI191107-A2.

XX 27-MAR-2002.

XX 21-AUG-2001; 2001EP-00250300.

XX 25-SBP-2000; 2000DB-01048633.

XX

PA (SCHD ) SCHERING AG.

XX Hess-Stump H, Haendler B, Kraetzschmar J, Krefz B, Winterhager B;  
XX PI Regidor P, Scotti S;

XX WPI; 2002-317413/36.

XX In vitro diagnosis and monitoring of endometriosis, comprises detecting  
XX PT reduced expression of specific gene products, e.g. from the fibronectin  
XX PT gene.

XX Claim 1; Page 15-16; 21pp; German.

XX The present invention relates to a method for the in vitro diagnosis of  
XX CC endometriosis by determining the amount of gene product from at least one  
XX CC specific gene in a patient sample and comparing this with the amount of  
XX CC gene product in a control sample. A reduced level is indicative of  
XX CC endometriosis. The gene products may be fibronectin, p27, reticulocalbin,  
XX CC aldehyde dehydrogenase 6, gravin, phospholipase C epsilon, elastin,  
XX CC insulin-like growth factor binding protein-2, alpha-2 type IV collagen,  
XX CC transmembrane receptor PTK7, collagen type XVIII alpha 1, platelet  
XX CC derived growth factor receptor alpha, laminin M chain, subtilisin like  
XX CC protein PACE4 or nidogen. The method is useful for initial diagnosis of  
XX CC endometriosis, and also for monitoring progress and treatment of the  
XX CC disease. The present sequence is human elastin

SQ Sequence 730 AA;

Query Match 98.3%; Score 515; DB 5; Length 730;  
Best Local Similarity 100.0%; Pred. No. 4e-35;  
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPGAI PGCVPGCVFPFGAGLGLAGLGGALGPGGKPLKVPVPGIAGAGLGAFAFPAVT 62  
DB 27 GGVPGAI PGCVPGCVFPFGAGLGLAGLGGALGPGGKPLKVPVPGIAGAGLGAFAFPAVT 86

QY 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100  
DB 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 124

## RESULT 13

ADQ19747  
ID ADQ19747 standard; protein; 730 AA.

XX ADQ19747;

DT 26-AUG-2004 (first entry)

XX Human soft tissue sarcoma-upregulated protein - SEQ ID 2566.

XX soft tissue sarcoma; cytoskeletal; gene therapy; vaccine; screening; human.

XX Homo sapiens.

XX WO2004048938-A2.

XX 10-JUN-2004.

XX 26-NOV-2003; 2003WO-US038193.

XX 26-NOV-2002; 2002US-0429739P.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Aziz N, Ginsburg WM, Zlotnick A;

XX WPI; 2004-441208/41.

XX Early detection of soft tissue sarcoma comprises determining expression  
XX PT of a gene in a first soft tissue sample and a normal soft tissue sample  
XX PT and comparing the gene expression, also useful in treating soft tissue  
XX PT sarcoma.

XX Example 2; SEQ ID NO 2566; 210pp; English  
PS

The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual, and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytosolic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.

**SQ** Sequence 730 AA;

Query Match	98.3%;	Score 515;	DB 8;	Length 730;
Best Local Similarity	100.0%;	Pred. No. 4e-35;		
Matches 98; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 3 GGVPGAI PGGVPGGVFYFPGAGLGLGGALGPCKPLKPVPGGLAGLGLGAEPAVT 622  
|||||  
Db 27 GGVPGAI PGGVPGGVFYFPGAGLGLGGALGPCKPLKPVPGGLAGLGLGAEPAVT 866

<b>QY</b>	63	PFGALVPGGVADAAAYKAKAGAGLGVPVGGLGVS	100
<b>Dδ</b>	87	PFGALVPGGVADAAAYKAKAGAGLGVPVGGLGVS	124

RESULT 14  
AAy69068  
ID AAy69068 standard; protein; 731 AA

AC	AAV69068;
XX	
DT	30-MAY-2000 (first entry)

DE Amino acid sequence of a human tropoelastin splice form

KW Tropolactasin; derivative; proteolysis; protease; antiwrinkle;  
 KW hand lotion; bulking agent; chamotaxis; proliferation; growth inhibition;  
 KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting

OS Homo sapiens.

FT	Key	Location/Qualifiers
FT	Cleavage-site	441. .442
FT	Cleavage-site	503. .504
FT	Cleavage-site	515. .516
FT	Cleavage-site	564. .565

PN WO200004043-A1.

PD 27-JAN-2000.

PF 19-JUL-1999; 99WO-AU000580.

PR 17-JUL-1998; 98AU-00004723.

PA (UNSY ) UNIV SYDNEY.

PI Weiss AS;

DR WPI; 2000-182399/16.

XX

PT cell growth.

PS Disclosure; Page 107-109; 136pp; English.

XX The present sequence represents a human tropoelastin splice form. The  
CC specification describes tropoelastin derivatives, in which a subsequence  
CC has been mutated so that susceptibility to proteolysis is reduced or  
CC eliminated, or a subsequence has been inserted so that susceptibility to  
CC proteolysis is increased. The derivatives have with reduced  
CC susceptibility, and can be used where the wild-type protein would be  
CC degraded too easily, e.g. in contact with serum or wound exudate. The  
CC tropoelastin derivatives provide competitive inhibition of protease  
CC activity. The tropoelastin derivatives, and other polypeptides containing  
CC tropoelastin derivative-derived protease-susceptibility sites, are useful  
CC in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hard  
CC lotions), as bulking agents and for inducing chemotaxis. They are also  
CC useful for proliferation or growth inhibition, particularly of smooth  
CC muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes,  
CC chondrocytes and platelets. Peptidomimetics that mimic the protease  
CC cleavage site in tropoelastin derivatives are competitive inhibitors of  
CC the protease, and are used for protecting against lung damage caused by  
CC elastin, for inhibiting or controlling localized growth of cancers or  
CC metastases, or to limit protease activity that causes blood clotting  
XX  
SQ Sequence 731 AA;

Query Match	98.3%	Score 515	DB 3	Length 731
Best Local Similarity	100.0%	Pred. NC. 4e-35		
Matches 98	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy 3 GGVPGAI PGVPGGVFY PGAGLGLGCGALGPGGKPLKPY PGGLAGAGLGGATPAAVT 62

Db 1 GGVPGAI PGVPGGVFY PGAGLGLGCGALGPGGKPLKPY PGGLAGAGLGGATPAAVT 60

QY	63	FP	GA	LV	PG	SV	AD	AA	AA	YK	AK	AG	AG	LG	GV	PG	VG	GL	GV	100
Db	61	FP	GA	LV	PG	SV	AD	AA	AA	YK	AK	AG	AG	LG	GV	PG	VG	GL	GV	98

RESULT 15  
AAB66657  
ID AAB66657 standard; protein; 731 AA

AC    AAB66657;

DT	05-APR-2001 (first entry)
XX	
DE	Human elastin protein without signal peptide

KW Minimal funct

OS Homo sapiens.

PN WO2001.00666.

PD 04-JAN-2001.

PF 29-JUN-2000; 2000WO-US017829.

PR 29-JUN-1999; 99US-00340736.

PA (PROT-) PROTEIN SPECIALTY

XX

XX

XX

PT and are not naturally occurring

PS Claim 1; Fig 1; 39pp; English.



CC prosthetic material such as prosthesis for blood vessel replacements, for  
CC heart valve replacement, tissue replacement, for covering burns, for  
CC covering wounds and stents  
XX  
SQ Sequence 731 AA;

Query Match 98.3%; Score 515; DB 4; Length 731;  
Best Local Similarity 100.0%; Pred. No. 4e-35; Indels 0; Gaps 0;  
Matches 98; Conservative 0; Mismatches 0;  
QY 3 GGVPGAI PGGVPGGVFPYPGAGLGGALGGALPGGKPLKVPYGGIAGAGLGAFFPAVT 62  
DB 1 GGVPGAI PGGVPGGVFPYPGAGLGGALGGALPGGKPLKVPYGGIAGAGLGAFFPAVT 60  
QY 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGIGVS 100  
DB 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGIGVS 98

Search completed: August 10, 2005, 07:33:50  
Job time : 121.905 secs

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GenCore Version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: August 10, 2005, 07:27:07 ; Search time 29.8507 Seconds  
(without alignments)  
250.074 Million cell updates/sec

Title: US-09-743-818A-4\_COPY\_1\_100

Perfect score: 524  
Sequence: 1 SMGVPGALPGVPGVFPV.....AAKAGLGSGVPGVGLGVS 100

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5E\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	524	100.0	733	3	US-08-464-700-2
2	515	98.3	730	4	US-09-961-403-8
3	515	98.3	731	2	US-08-911-364-1
4	515	98.3	731	4	US-09-340-736E-1
5	515	98.3	731	4	US-09-964-662-1
6	515	98.3	732	2	US-08-678-039A-40
7	177.5	33.9	479	1	US-08-397-633A-78
8	174	33.2	832	1	US-08-212-237-4
9	174	33.2	832	3	US-08-806-029-27
10	174	33.2	832	5	PCT-US95-02772-4
11	174	33.2	936	2	US-08-707-237A-108
12	174	33.2	936	4	US-08-642-246-30
13	174	33.2	936	3	US-09-451-206-30
14	174	33.2	936	5	PCT-US96-06229-30
15	173	33.0	312	3	US-08-806-029-34
16	173	33.0	378	2	US-08-707-237A-104
17	173	33.0	378	3	US-08-642-246-26
18	173	33.0	378	4	US-09-451-206-26
19	173	33.0	378	5	PCT-US96-06229-26
20	173	33.0	936	1	US-08-212-237-3
21	173	33.0	936	3	US-08-806-029-26
22	173	33.0	936	5	PCT-US95-02772-3
23	173	33.0	1002	2	US-08-707-237A-103
24	173	33.0	1002	3	US-08-642-246-25
25	173	33.0	1002	4	US-09-451-206-25
26	173	33.0	1002	5	PCT-US96-06229-25
27	172	32.8	486	1	US-08-397-633A-77

28	171	32.6	262	1	US-08-397-633A-73	Sequence 73, Appl
29	168	32.1	696	3	US-08-806-029-36	Sequence 36, Appl
30	168	32.1	750	3	US-08-806-029-25	Sequence 25, Appl
31	167.5	32.0	251	1	US-08-397-633A-74	Sequence 74, Appl
32	166	31.7	1413	1	US-08-175-155-39	Sequence 39, Appl
33	166	31.7	1413	2	US-08-707-237A-45	Sequence 45, Appl
34	166	31.7	1464	1	US-08-477-509B-74	Sequence 74, Appl
35	166	31.7	1464	3	US-08-482-085B-74	Sequence 74, Appl
36	166	31.7	1465	3	US-09-444-791A-74	Sequence 74, Appl
37	164	31.3	988	1	US-08-212-237-5	Sequence 5, Appl
38	164	31.3	988	3	US-08-806-029-28	Sequence 28, Appl
39	164	31.3	988	5	PCT-US95-02772-5	Sequence 5, Appl
40	162.5	31.0	287	1	US-08-397-633A-76	Sequence 76, Appl
41	162	30.9	281	1	US-08-397-633A-75	Sequence 75, Appl
42	161.5	30.8	768	3	US-08-806-029-35	Sequence 35, Appl
43	161.5	30.8	877	1	US-08-397-633A-54	Sequence 54, Appl
44	161.5	30.8	884	1	US-08-397-633A-68	Sequence 68, Appl
45	161.5	30.8	884	2	US-08-435-641-15	Sequence 15, Appl

## ALIGNMENTS

RESULT 1  
US-08-464-700-2  
Sequence 2, Application US/08464700  
Patent No. 6232458  
GENERAL INFORMATION:  
APPLICANT: WEISS, ANTHONY S  
APPLICANT: MARTIN, STEPHEN L  
TITLE OF INVENTION: SYNTHETIC POLYNUCLEOTIDES  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESS: Howson and Howson  
STREET: Spring House Corporate Cntr, PO Box 457  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,700  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PL6520  
FILING DATE: 22-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PL9661  
FILING DATE: 28-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/AU93/00655  
FILING DATE: 16-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: GHCUUSA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-540-9200  
TELEFAX: 215-540-5818  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 733 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-700-2  
Query Match 100.0%; Score 524; DB 3; Length 733;

Best Local Similarity 100.0%; Pred. No. 2,3e-38;  
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SMGVPGAIPEGVPGVFPFGAGLGGALGPGGKPLKVPVPGLAGAGLAGAPAVT 60

DB 1 SMGVPGAIPEGVPGVFPFGAGLGGALGPGGKPLKVPVPGLAGAGLAGAPAVT 60

QY 61 VTFPGALVPGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100  
DB 61 VTFPGALVPGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100

## RESULT 2

US-09-961-403-8  
Sequence 8, Application US/09961403

Patent No. 6780394

GENERAL INFORMATION:

APPLICANT: HE-STUMP, HOLGER

APPLICANT: HAENDLER, BERNARD

APPLICANT: KRAETZSCHMAR, JOERN

APPLICANT: KREFT, BERTHOLT

APPLICANT: WINTERHAGER, ELKE

APPLICANT: REGIDOR, PEDRO

APPLICANT: SCOTTI, SIMONE

TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS

FILE REFERENCE: SCH-1789

CURRENT APPLICATION NUMBER: US/09/961,403

CURRENT FILING DATE: 2001-09-25

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 8

LENGTH: 730

TYPE: PRT

ORGANISM: Homo sapiens

US-09-961-403-8

Query Match 98.3%; Score 515; DB 4; Length 730;  
Best Local Similarity 100.0%; Pred. No. 1.4e-37;

Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPGAIPGCVPGVFPFGAGLGGALGPGGKPLKVPVPGLAGAGLAGAPAVT 62

DB 27 GGVPGAIPGCVPGVFPFGAGLGGALGPGGKPLKVPVPGLAGAGLAGAPAVT 86

QY 63 FPGALVPGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100  
DB 87 FPGALVPGVADAAAAYKAAKAGAGLGGVPGVGLGVS 124

## RESULT 3

US-08-911-364-1  
Sequence 1, Application US/08911364

Patent No. 5969106

GENERAL INFORMATION:

APPLICANT: ROTHSTEIN, ASER

APPLICANT: KEELY, Fred W.

APPLICANT: ROTHSTEIN, Steven J.

TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN

TITLE OF INVENTION: ELASTIN AND OTHER FIBROUS PROTEINS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESSES:

ADDRESSEE: FOLEY & LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

APPLICATION NUMBER: US/08/911,364  
FILING DATE: 07-AUG-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/023,552

FILING DATE: 07-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 041082/0104

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 731 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-911-364-1

Query Match 98.3%; Score 515; DB 2; Length 731;  
Best Local Similarity 100.0%; Pred. No. 1.4e-37;

Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPGAIPGCVPGVFPFGAGLGGALGPGGKPLKVPVPGLAGAGLAGAPAVT 62

DB 1 GGVPGAIPGCVPGVFPFGAGLGGALGPGGKPLKVPVPGLAGAGLAGAPAVT 60

QY 63 FPGALVPGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100  
DB 61 FPGALVPGVADAAAAYKAAKAGAGLGGVPGVGLGVS 98

## RESULT 4

US-09-340-736E-1  
Sequence 1, Application US/09340736E

Patent No. 6489446

GENERAL INFORMATION:

APPLICANT: ROTHSTEIN, ASER

APPLICANT: KEELY, FRED

APPLICANT: ROTHSTEIN, STEVEN

TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN

TITLE OF INVENTION: AND OTHER FIBROUS PROTEINS

FILE REFERENCE: 041082/0110

CURRENT APPLICATION NUMBER: US/09/340,736E

CURRENT FILING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: 08/911,364

PRIOR FILING DATE: 1997-08-07

PRIOR APPLICATION NUMBER: 60/023,552

PRIOR FILING DATE: 1996-08-07

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 731

TYPE: PRT

ORGANISM: Homo sapiens

US-09-340-736E-1

Query Match 98.3%; Score 515; DB 4; Length 731;  
Best Local Similarity 100.0%; Pred. No. 1.4e-37;

Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPGAIPGCVPGVFPFGAGLGGALGPGGKPLKVPVPGLAGAGLAGAPAVT 62

DB 1 GGVPGAIPGCVPGVFPFGAGLGGALGPGGKPLKVPVPGLAGAGLAGAPAVT 60

QY 63 FPGALVPGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100  
DB 61 FPGALVPGVADAAAAYKAAKAGAGLGGVPGVGLGVS 98



Db 191 GVGVPGVGV 199

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RESULT 8
US-08-212-237-4
; Sequence 4, Application US/08212237
; Patent No. 5606019
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: Synthetic Proteins As Implantables
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,237
; FILING DATE: 11-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Beirtram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58847/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 832 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-212-237-4

Query Match 33.2%; Score 174; DB 1; Length 832;
Best Local Similarity 39.3%; Pred. No. 1.3e-07;
Matches 53; Conservative 6; Mismatches 32; Indels 44; Gaps 7;

QY 4 GVPG-AIPG-GVPG-----GVFPAGALGAGGALPGGKPLKPVPGIAGAGLGA 57
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 10 GVPGVGPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVP 64
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QY 58 FPAVTFPGALVPG-----GVADAAAYKA-----AKGA 86
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Db 65 VPGVGPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVP 124
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 87 GLGVPGVG--GLGV 99
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Db 125 GAGSVPGVGPVGVPV 139

RESULT 9
US-08-806-029-27
; Sequence 27, Application US/08806029
; Patent No. 6380154
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; APPLICANT: Steedronsky, Erwin R.
; TITLE OF INVENTION: Synthetic Proteins for in vivo Drug
; TITLE OF INVENTION: Delivery and Tissue Augmentation
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
```

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; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/806,029
; FILING DATE: 24-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,237
; FILING DATE: 11-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-58847-2/RFT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 832 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
;
US-08-806-029-27
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Query Match 33.2%; Score 174; DB 3; Length 832;
Best Local Similarity 39.3%; Pred. No. 1.3e-07;
Matches 53; Conservative 6; Mismatches 32; Indels 44; Gaps 7;

QY 4 GVPG-AIPG-GVPG-----GVFPAGALGAGGALPGGKPLKPVPGIAGAGLGA 57
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Db 10 GVPGVGPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVP 64
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QY 58 FPAVTFPGALVPG-----GVADAAAYKA-----AKGA 86
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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QY 87 GLGVPGVG--GLGV 99
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Db 125 GAGSVPGVGPVGVPV 139

RESULT 10
PCT-US95-02772-4
; Sequence 4, Application PC/TUS9502772
; GENERAL INFORMATION:
; APPLICANT: Protein Polymer Technologies, Inc.
; TITLE OF INVENTION: Synthetic Proteins As Implantables
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02772
; FILING DATE:
; CLASSIFICATION:
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FILING DATE: 09-NOV-

TELEPHONE: 415-781-  
TELEFAX: 415-398-32

TELEFAX: 415-398-32

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QY      58  --FPAVTFPGALVPGGVADAAALYKAAKAGAGLG-----GVPGVG--GLGV  99
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RESULT 15
US-08-806-029-34
; Sequence 34, Application US/08806029
; Patent No. 6380154
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; APPLICANT: Steadronsky, Erwin R.
; TITLE OF INVENTION: Synthetic Proteins for in vivo Drug
; TITLE OF INVENTION: Delivery and Tissue Augmentation
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fleht, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/806.029
; FILING DATE: 24-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,237
; FILING DATE: 11-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Treacartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-58847-2/RT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-806-029-34

Query Match          33.0%; Score 173; DB 3; Length 312;
Best Local Similarity 36.1%; Pred. No. 5.9e-08;
Matches 57; Conservative 7; Mismatches 32; Indels 62; Gaps 8;

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QY 44 G-----GLAGGLAGLGA-----FPATFPAL 67
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DB 90 GVGVPGVGPVGPVGPAGAGSGAGSGVGPVGPVGPVGPVGPVGPVGP 149
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QY 68 VPGGVADAAAYKAKAGAGL---GVPGV---GLGV 99
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DB 150 VPGVGPAGAGSGAGSGVGPVGPVGPVGPVGPVGPVGPVGPVGPV 187
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Job time : 30.8507 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: August 10, 2005, 07:37:53 ; Search time 104.478 Seconds  
(without alignments)  
373.667 Million cell updates/sec

Title: US-09-743-818a-4\_COPY\_1\_100

Perfect score: 524  
Sequence: 1 SMGCVPGAIIPGVGVGVFYP.....AAKAGAGLGCVPGVGLGVIS 100Scoring table: BLOSUM62  
Gapco 10.0 , Gapext 0.5

Searched: 1752860 seqs, 390397842 residues

Total number of hits satisfying chosen parameters: 1752860

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications AA:\*

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3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

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14: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*

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18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*

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21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	515	98.3	692	15	Sequence 40, Appl
2	515	98.3	711	15	Sequence 38, Appl
3	515	98.3	730	10	Sequence 8, Appl
4	515	98.3	730	16	Sequence 2566, Ap
5	515	98.3	731	10	Sequence 1, Appl
6	515	98.3	788	16	Sequence 4, Appl
7	515	98.3	788	16	Sequence 3, Appl
8	448	85.5	617	15	Sequence 2915, Ap
9	334.5	63.8	663	15	Sequence 2477, Ap
10	174	33.2	832	8	Sequence 27, Appl
11	174	33.2	936	14	Sequence 30, Appl

12	173	33.0	312	8	US-08-806-029-34
13	173	33.0	378	14	US-10-117-931-26
14	173	33.0	936	8	US-08-806-029-26
15	173	33.0	1002	14	US-10-117-931-25
16	168	32.1	696	8	US-08-806-029-36
17	168	32.1	696	15	US-10-441-965-23
18	168	32.1	750	8	US-08-806-029-25
19	166	31.7	1465	14	US-10-096-986-74
20	165.5	31.6	696	15	US-10-441-965-21
21	164	31.3	562	16	US-10-720-025-32
22	164	31.3	730	16	US-10-720-025-35
23	164	31.3	988	8	US-08-806-029-28
24	164	31.3	1382	16	US-10-720-025-60
25	164	31.3	1550	16	US-10-720-025-54
26	163	31.1	450	9	US-09-812-382-6
27	161.5	30.8	244	16	US-10-800-179-27
28	161.5	30.8	244	16	US-10-845-775A-27
29	161.5	30.8	244	16	US-10-845-936A-27
30	161.5	30.8	244	18	US-10-939-036-27
31	161.5	30.8	246	16	US-10-800-179-26
32	161.5	30.8	246	16	US-10-800-179-28
33	161.5	30.8	246	16	US-10-845-775A-26
34	161.5	30.8	246	16	US-10-845-775A-28
35	161.5	30.8	246	16	US-10-845-936A-26
36	161.5	30.8	246	16	US-10-845-936A-28
37	161.5	30.8	246	18	US-10-939-036-26
38	161.5	30.8	246	18	US-10-939-036-28
39	161.5	30.8	768	8	US-08-806-029-35
40	161.5	30.8	884	14	US-10-117-931-15
41	161.5	30.8	889	8	US-08-806-029-19
42	161.5	30.8	983	16	US-10-845-936A-37
43	161.5	30.8	1027	16	US-10-845-936A-32
44	161.5	30.8	1105	16	US-10-845-936A-33
45	161.5	30.8	1125	16	US-10-845-936A-34

## ALIGNMENTS

Sequence 34, Appl  
Sequence 26, Appl  
Sequence 26, Appl  
Sequence 25, Appl  
Sequence 36, Appl  
Sequence 23, Appl  
Sequence 25, Appl  
Sequence 74, Appl  
Sequence 21, Appl  
Sequence 33, Appl  
Sequence 35, Appl  
Sequence 28, Appl  
Sequence 60, Appl  
Sequence 54, Appl  
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Sequence 15, Appl  
Sequence 19, Appl  
Sequence 32, Appl  
Sequence 37, Appl  
Sequence 33, Appl  
Sequence 34, Appl

RESULT 1  
US-10-210-172-40  
; Sequence 40, Application US/10210172  
; Publication No. US20040043928A1  
GENERAL INFORMATION:  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Miller, Charles  
; APPLICANT: Paturajan, Meera  
; APPLICANT: Pena, Carol  
; APPLICANT: Rieger, Daniel  
; APPLICANT: Shimkets, Richard  
; APPLICANT: Zernhusen, Bryan  
; APPLICANT: Li, Li  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Casman, Stacie  
; APPLICANT: Voss, Edward  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Gorman, Linda  
; APPLICANT: Leite, Mario  
; APPLICANT: Vernet, Corine  
; APPLICANT: Anderson, David  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Zhong, Mei  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Hjalte, Tord  
; APPLICANT: Raetelli, Luca  
; APPLICANT: Szytek, Kimberly  
; APPLICANT: Edinger, Shlomit  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Malyankar, Uriel  
; APPLICANT: MacDougall, John  
; APPLICANT: Stone, David  
; APPLICANT: Alebrock II, John

```
APPLICANT: Lepley, Denise et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-416 A
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/309,501
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/323,994
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/373,814
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/310,291
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 60/310,951
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/310,544
PRIOR FILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: 60/311,292
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/311,979
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 60/313,201
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/312,892
PRIOR FILING DATE: 2001-08-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 327
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 40
LENGTH: 692
TYPE: PRT
ORGANISM: Homo sapiens
US-10-210-172-40
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Query Match      98.3%; Score 515; DB 15; Length 692;
Best Local Similarity 100.0%; Pred. No. 1.9e-31;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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## RESULT 2

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US-10-210-172-38
Sequence 38, Application US/10210172
Publication No. US20040043928A1
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## GENERAL INFORMATION:

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APPLICANT: Kekuda, Rameesh
APPLICANT: Miller, Charles
APPLICANT: Patuturajan, Meera
APPLICANT: Pena, Carol
APPLICANT: Rieger, Daniel
APPLICANT: Shimkets, Bryan
APPLICANT: Zehrusen, Bryan
APPLICANT: Li, Li
APPLICANT: Uj, Weizhen
APPLICANT: Padigar, Muralidhara
APPLICANT: Casman, Stacie
APPLICANT: Voss, Edward
APPLICANT: Boldog, Ferenc
APPLICANT: Gorman, Linda
APPLICANT: Leite, Mario
APPLICANT: Vermet, Corine
APPLICANT: Anderson, David
APPLICANT: Guo, Xiaojia
APPLICANT: Zhong, Wei
APPLICANT: Gerlach, Valerie
APPLICANT: Hjalte, Tord
```

```
APPLICANT: Rastelli, Luca
APPLICANT: Spytek, Kimberly
APPLICANT: Edinger, Shlomit
APPLICANT: Ellerman, Karen
APPLICANT: Malpankar, Uriel
APPLICANT: MacDougall, John
APPLICANT: Stone, David
APPLICANT: Alsebrook II, John
APPLICANT: Lepley, Denise et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-416 A
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/309,501
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/323,994
PRIOR FILING DATE: 2001-09-21
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PRIOR APPLICATION NUMBER: 60/311,292
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/311,979
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 60/313,201
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/312,892
PRIOR FILING DATE: 2001-08-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 327
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 38
LENGTH: 711
TYPE: PRT
ORGANISM: Homo sapiens
US-10-210-172-38
```

```
Query Match      98.3%; Score 515; DB 15; Length 711;
Best Local Similarity 100.0%; Pred. No. 1.9e-31;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      3 GGVPGAIIPGVPGVYPPAGLGGALGPGKPLKVPGLAGAGLGAAPPAVT 62
      |||
DB      27 GGVPGAIIPGVPGVYPPAGLGGALGPGKPLKVPGLAGAGLGAAPPAVT 86
      |||

QY      63 FPGALVPGGVADAAAYKAAKAGAGLGVPGVGLGVS 100
      |||
DB      87 FPGALVPGGVADAAAYKAAKAGAGLGVPGVGLGVS 124
      |||
```

## RESULT 3

```
US-09-961-403-8
Sequence 8, Application US/09961403
Publication No. US20030077589A1
```

## GENERAL INFORMATION:

```
APPLICANT: HE-STUMP, HOLGER
APPLICANT: HAENDLER, BERNARD
APPLICANT: KRAETZSCHMAR, JOERN
APPLICANT: KREFT, BERTHOLT
APPLICANT: WINTERHAGER, ELKE
APPLICANT: REGIDOR, PEDRO
APPLICANT: SCOTTI, SIMONE
TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
FILE REFERENCE: SCH-1789
CURRENT APPLICATION NUMBER: US/09/961,403
CURRENT FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
```



```
/ TITLE OF INVENTION: Stimulation of the activity of an isoform of lysyl oxidase
/ TITLE OF INVENTION: for combating against some pathologies due to an incomplete,
/ FILE REFERENCE: 11123.82US01
/ CURRENT APPLICATION NUMBER: US/10/852,575
/ PRIOR FILING DATE: 2004-05-24
/ PRIOR APPLICATION NUMBER: FR 03 07178
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3
/ LENGTH: 788
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-852-575-3

Query Match          98.3%; Score 515; DB 16; Length 788;
Best Local Similarity 100.0%; Pred. No. 2.1e-31;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPAIPGGVPGVFPYPGAGLGGALGPGKPLKRVPGGLAGAGLGAFFPAVT 62
DB 27 GGVPAIPGGVPGVFPYPGAGLGGALGPGKPLKRVPGGLAGAGLGAFFPAVT 86
QY 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100
DB 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 124

RESULT 8
US-10-104-047-2915
/ Sequence 2915, Application US/10104047
/ Publication No. US20030236392A1
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: NO. US20030236392A1e1 full length cDNA
/ FILE REFERENCE: H1-A0105
/ CURRENT APPLICATION NUMBER: US/10/104,047
/ PRIOR FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER:
/ NUMBER OF SEQ ID NOS: 4096
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2915
/ LENGTH: 617
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-104-047-2915

Query Match          85.5%; Score 448; DB 15; Length 617;
Best Local Similarity 89.8%; Pred. No. 2.2e-26;
Matches 88; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 GGVPAIPGGVPGVFPYPGAGLGGALGPGKPLKRVPGGLAGAGLGAFFPAVT 62
DB 27 GGVPAIPGGVPGVFPYPGAGLGGALGPGKPLKRVPGGLAGAGLGAFFPAVT 76
QY 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100
DB 77 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 114

RESULT 9
US-10-108-260A-2477
/ Sequence 2477, Application US/10108260A
/ Publication No. US20040005560A1
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: NO. US20040005560A1e1 full length cDNA
/ FILE REFERENCE: H1-A0106
/ CURRENT APPLICATION NUMBER: US/10/108,260A
/ PRIOR FILING DATE: 2002-03-27
/ NUMBER OF SEQ ID NOS: 5458
```

```
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2477
/ LENGTH: 663
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-108-260A-2477

Query Match          63.8%; Score 334.5; DB 15; Length 663;
Best Local Similarity 68.4%; Pred. No. 1.1e-17;
Matches 67; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

QY 3 GGVPAIPGGVPGVFPYPGAGLGGALGPGKPLKRVPGGLAGAGLGAFFPAVT 62
DB 27 GGVPAIPGGVPGVFPYPGAGLGGALGPGKPLKRVPGGLAGAGLGAFFPAVT 76
QY 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100
DB 77 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 93

RESULT 10
US-08-806-029-27
/ Sequence 27, Application US/08806029
/ Publication No. US20020045567A1
/ GENERAL INFORMATION:
/ APPLICANT: Cappello, Joseph
/ APPLICANT: Stedronsky, Erwin R.
/ TITLE OF INVENTION: Synthetic Proteins for in vivo Drug
/ TITLE OF INVENTION: Delivery and Tissue Augmentation
/ NUMBER OF SEQUENCES: 36
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
/ STREET: Four Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/806,029
/ FILING DATE: 24-FEB-1997
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/212,237
/ FILING DATE: 11-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Trecartin, Richard F.
/ REGISTRATION NUMBER: 31,801
/ REFERENCE/DOCKET NUMBER: A-58847-2/RFT/MTK
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 781-1989
/ TELEFAX: (415) 398-3249
/ INFORMATION FOR SEQ ID NO: 27:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 832 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
US-08-806-029-27

Query Match          33.2%; Score 174; DB 8; Length 832;
Best Local Similarity 39.3%; Pred. No. 2.3e-05;
Matches 53; Conservative 6; Mismatches 32; Indels 44; Gaps 7;

QY 4 GVPG-AIRG-GVPG-----GVFPYPGAGLGGALGPGKPLKRVPGGLAGAGLGA 57
DB 10 GVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 64
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```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/806,029
FILING DATE: 24-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,237
FILING DATE: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Treccartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58847-2/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1589
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 936 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-806-029-26

Query Match          33.8%; Score 173; DB 8; Length 936;
Best Local Similarity 34.8%; Pred. No. 3e-05;
Matches 55; Conservative 6; Mismatches 35; Indels 62; Gaps 7

QY      4  GVPG-AIPG-GVPG-----GVFYPGAGLGLGCGALVPG----- 35
      |||  :||  :||  :||  :||  :||  :||  :||  :||  :||
Db      10  GVPGVGVPGVGVPGVGVPGVGVPGVGVGAGAGSGAGSGVPGVGVPGVGVPGV 69
      |||  :||  :||  :||  :||  :||  :||  :||  :||  :||

QY      36  -----GPELRVPG-GIAGAGLGIAGAFPAVTFPGALVPG----- 70
      |||  :||  :||  :||  :||  :||  :||  :||  :||  :||
Db      70  -----GPELRVPG-GIAGAGLGIAGAFPAVTFPGALVPG----- 129
      |||  :||  :||  :||  :||  :||  :||  :||  :||  :||

```

```

Query Match      33.0%; Score 173; DB 8; Length 936;
Best Local Similarity 34.8%; Pred. No. 3e-05;
Matches 55; Conservative 6; Mismatches 35; Indels 62; Gaps 7

QY          4 GVPG-AIPG-GVPP-----GVFPYGAGLGCALGGALPGP----- 35
           ||||| :||| |::| |::| |
Db          10 GVPGVGPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVP 69
               -----GKPLRPVG-GLAGAGLGAGLAFPAVTPGALVPG----- 70
QY          36 ----- 70
           70 GVPVPVGVPVGVPVGVPVGVPVGAGAGSGAGAGSPVGPVGVPVGVPVG 129
QY          71 -----GVADAAAATRAAKAGAGLGGVPVG--GLGV 99
           ||||| :||| |::| |::| |
Db          130 VPGVPVGVPVGVPVGAGAGSGAGAGSGVPVGVPVGVP 167

RESULT 15
US-10-117-931-25
Sequence 25, Application US/10117931
Publication No. US20030104589A1
GENERAL INFORMATION:
APPLICANT: STEDRONSKY, Erwin R.
CAPPELO, Joseph
TITLE OF INVENTION: Tissue Adhesive Using Synthetic
Crosslinking

```

RESULT 15  
US-10-117-931-25  
Sequence 25, Application US/10117931  
Publication No. US20030104589A1  
GENERAL INFORMATION:  
APPLICANT: STEDRONSKY, Erwin R.  
CAPPELLO, Joseph  
TITLE OF INVENTION: Tissue Adhesive Using Synthetic  
Crosslinking  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOENBACH, TEST, ALBERTSON & HERBERT  
STREET: Four Embarcadero Center, Suite 200  
CITY: San Francisco  
STATE: CA  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/117,931  
FILING DATE: 05-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/642,246  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: ROWLAND, Bertram I  
REGISTRATION NUMBER: 20015  
REFERENCE/DOCKET NUMBER: A61127-1/BIR







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 10, 2005, 07:25:52 ; Search time 24.3781 Seconds  
(Without alignments)  
394.685 Million cell updates/sec

Title: US-09-743-818A-4\_COPY\_1\_100

Perfect score: 524  
Sequence: 1 SMGVPGALPGVPGVFP.....AAKAGAGLGVPVGLGVS 100

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	515	98.3	792	1	EAHU
2	377	71.9	860	1	EAMS
3	326.5	62.3	864	1	EART
4	326	62.2	770	2	S59623
5	324.5	61.9	747	1	EABO
6	310	59.2	784	2	A26601
7	148	28.2	158	2	T08957
8	148	28.2	735	2	T05389
9	146.5	28.0	212	2	E86179
10	144.5	27.6	641	1	Q08B31
11	141	26.9	376	2	T10455
12	136.5	26.0	767	2	E70855
13	136	26.0	447	2	G84687
14	136	26.0	1489	2	D70807
15	136	26.0	1901	2	T05442
16	135	25.8	608	2	F70806
17	134.5	25.7	907	2	A45560
18	133.5	25.5	882	2	B70812
19	132.5	25.3	162	2	S56703
20	131	25.0	338	1	KNMU
21	131	25.0	384	1	A26099
22	130.5	24.9	718	2	A36068
23	129.5	24.7	543	2	F70726
24	128.5	24.5	132	2	S14977
25	127.5	24.3	87	2	T14302
26	127.5	24.3	2038	2	A43762
27	127	24.2	210	2	J01060
28	127	24.2	783	2	E70824
29	125.5	24.0	925	2	JC2033

30	125	23.9	1147	1	MMAX1B	myosin heavy chain
31	124.5	23.8	307	2	T27609	hypothetical prote
32	124.5	23.7	749	2	A70812	hypothetical glyci
33	124	23.7	228	2	T49891	glycine-rich prote
34	124	23.7	515	2	H70663	hypothetical glyci
35	124	23.7	778	2	F70963	hypothetical glyci
36	124	23.7	1660	2	A70869	hypothetical glyci
37	123.5	23.6	479	2	F70573	hypothetical prote
38	123.5	23.6	512	2	S70644	annexin VII - Afri
39	123	23.5	201	2	T00799	hypothetical prote
40	123	23.5	256	2	A70514	hypothetical glyci
41	122.5	23.4	271	2	S34666	glycine-rich prote
42	122.5	23.4	603	2	A70770	hypothetical glyci
43	121.5	23.2	112	2	J01063	glycine-rich prote
44	121.5	23.2	173	2	J01064	glycine-rich prote
45	121.5	23.2	220	2	T14441	glycine-rich prote

## ALIGNMENTS

## RESULT 1

EAHU

elastin precursor, long splice form - human  
N:Alternate names: tropoelastin

C:Species: Homo sapiens (man)  
C>Date: 22-Jun-1990 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004

C/Accession: A32707; A33705; A30524; A53891  
R:Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Sheppard, P.; Anderson, N.; Rosenblum, J

Proc. Natl. Acad. Sci. U.S.A. 84, 5680-5684, 1987  
A:Title: Alternative splicing of human elastin mRNA indicated by sequence analysis of c

A:Reference number: A32707; PMID:87289668; PMID:3039501  
A:Accession: A32707

A:Molecule type: mRNA  
A:Residues: 1-500,507-792 <IND>

A:Cross-references: UNIPROT:P15502; UNIPROT:Q9UMK5; GB:M16983; GB:J02948  
R:Barshir, M.M.; Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Rosenblum, J.C.; Abrams, W

J. Biol. Chem. 264, 8887-8891, 1989  
A:Title: Characterization of the complete human elastin gene. Delineation of unusual fe

A:Reference number: A33705; PMID:8925358; PMID:2722804  
A:Accession: A33705

A:Molecule type: DNA  
A:Residues: 1-27 <BAS>

A:Cross-references: GB:J04821; NID:G182052; PIDN:AA52379.1; PID:G553276  
R:Fezio, M.J.; Olsen, D.R.; Kaun, E.R.; Baldwin, C.T.; Indik, Z.; Ornstein-Goldstein, N

J. Invest. Dermatol. 91, 458-464, 1988  
A:Title: Cloning of full-length elastin cDNAs from a human skin fibroblast recombinant

A:Reference number: A30524; PMID:8900960; PMID:3171221  
A:Accession: A30524

A:Molecule type: mRNA  
A:Residues: 1-453,483-617,651-792 <FAZ>

A:Cross-references: EMBL:M6860; NID:G182061; PIDN:AA52382.1; PID:G182062  
A>Note: This sequence represents a composite of several splice forms

R:Fezio, M.J.; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rosenblum, J.; I  
Lab. Invest. 58, 270-277, 1988

A:Title: Isolation and characterization of human elastin cDNAs, and age-associated vari  
A:Reference number: A53891; PMID:8156138; PMID:2831431

A:Accession: A53891  
A:Molecule type: mRNA

A:Residues: 164-453,483-500,507-617,651-792 <FA2>  
A:Cross-references: GB:M24782; NID:G182063; PIDN:AA53190.1; PID:G182064

C:Comment: The term tropoelastin refers to a soluble precursor form of the extracellular  
line oxidase activity.

C:Genetics:  
A:Gene: GDB:ELN

A:Cross-references: GDB:119107; OMIM:130160  
A:Map position: 7q11.23-7q11.23

C:Superfamily: elastin  
C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxyllysine

F/1-26/Domain: signal sequence #status predicted <SIG>  
F/27-792/Product: elastin #status predicted <MNT>

F/782-787/Disulfide bonds: #status predicted  
G protein-coupled

Query Match 98.3%; Score 515; DB 1; Length 792;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-30;  
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPGAIPEGVPGVYFPAGLGGALGPGKPLKVPGLAGAGLGAFAFPVNT 62  
 |||||  
 DB 27 GGVPGAIPEGVPGVYFPAGLGGALGPGKPLKVPGLAGAGLGAFAFPVNT 86  
 |||||  
 QY 63 FPGALVPGGVADAAAAYKAKAGAGLGGVPGVGGVGS 100  
 |||||  
 DB 87 FPGALVPGGVADAAAAYKAKAGAGLGGVPGVGGVGS 124  
 |||||

## RESULT 2

EAMS

elastin precursor - mouse  
 N/Alternate names: tropoelastin  
 C/Species: Mus musculus (house mouse)  
 C/Date: 18-Aug-1995 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004  
 C/Accession: A55721

R/Wyther, K.S.; Sechler, J.L.; Boyd, C.D.; Passmore, H.C.  
 Genomics 23, 125-131, 1994  
 A/Title: Use of an intron length polymorphism to localize the tropoelastin gene to mouse  
 A/Reference number: A55721; MUID:95130069; PMID:7829060  
 A/Accession: A55721

A/Molecule type: mRNA  
 A/Residues: 1-860 <MYD>  
 A/Cross-references: UNIPROT:P54320; GB:U08210; NID:g473273; PIDN:AAA80155.1; PID:g473274  
 C/Genetics:  
 A/Map position: 5

C/Superfamily: elastin  
 C/Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxyllysine  
 F/1-21/Domain: signal sequence #status predicted <SIG>  
 F/28-860/Product: elastin #status predicted <MAT>  
 F/850-855/Disulfide bonds: #status predicted

Query Match 71.9%; Score 377; DB 1; Length 860;  
 Best Local Similarity 72.6%; Pred. No. 1.7e-20;  
 Matches 82; Conservative 4; Mismatches 11; Indels 16; Gaps 5;

QY 3 GGVPGAIPEGVPGVYFPAGLGGALGPGKPLKVPGLAGAGL 50  
 |||||  
 DB 32 GAVPGGLPGVPGVYFPAGLGGALGPGKPLKVPGLAGAGL 91  
 |||||  
 QY 51 LGAGGAFPAVTFP--GALVPGGVADAAAAYK-AAKAGAGLGGVPGV-GGLGV 99  
 |||||  
 DB 92 PGGALGAFPAITFPGAGALVPGAGAAAAYKAAKAGAGLGGVPGVGV 144  
 |||||

## RESULT 3

EART

elastin precursor - rat  
 N/Alternate names: tropoelastin  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 11-Jan-1991 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004  
 C/Accession: A36106; A30878; A36523; S02173; I54172; I68505

R/Pierce, R.A.; Deak, S.B.; Stolle, C.A.; Boyd, C.D.  
 Biochemistry 29, 9677-9683, 1990  
 A/Title: Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning.  
 A/Reference number: A36106; MUID:91104868; PMID:1702999  
 A/Accession: A36106

A/Molecule type: mRNA  
 A/Residues: 1-864 <PIE>  
 A/Cross-references: UNIPROT:Q99372; GB:M60647; GB:J05292; NID:g207444; PIDN:AAA42269.1;  
 R/Deak, S.B.; Pierce, R.A.; Belisky, S.A.; Riley, D.J.; Boyd, C.D.  
 J. Biol. Chem. 263, 13504-13507, 1988

A/Title: Rat tropoelastin is synthesized from a 3.5-Kilobase mRNA.  
 A/Reference number: A30878; MUID:88330866; PMID:2971041  
 A/Accession: A30878

A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 781-864 <DEA>  
 A/Cross-references: GB:J04035; NID:g207442; PIDN:AAA42268.1; PID:g207443

R/Franzblau, C.; Pratt, C.A.; Faris, B.; Colaninno, N.M.; Offner, G.D.; Mogszyel Jr., P.  
 J. Biol. Chem. 264, 15115-15119, 1989  
 A/Title: Role of tropoelastin fragmentation in elastogenesis in rat smooth muscle cells.  
 A/Reference number: A36523; MUID:89359327; PMID:2768256

A/Accession: A36523  
 A/Molecule type: protein  
 A/Residues: 22-31 <FRA>  
 R/Rich, C.B.; Foster, J.A.  
 Arch. Biochem. Biophys. 268, 551-558, 1989  
 A/Title: Characterization of rat heart tropoelastin.  
 A/Reference number: S02173; MUID:89117149; PMID:2913947  
 A/Accession: S02173

A/Status: not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 71P, 369-545, 548-764, 770-864 <RIC>

A/Experimental source: heart  
 R/Pierce, R.A.; Alatawi, A.; Deak, S.B.; Boyd, C.D.  
 Genomics 12, 651-658, 1992

A/Title: Elements of the rat tropoelastin gene associated with alternative splicing.  
 A/Reference number: I54172; MUID:92241859; PMID:1572637  
 A/Accession: I54172

A/Status: translated from GB/EMBL/DBJ  
 A/Molecule type: DNA

A/Residues: 264-533 <RES>  
 A/Cross-references: GB:M86372; NID:g207455; PIDN:AAA42271.1; PID:g554527

A/Accession: I68505  
 A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA  
 A/Residues: 558-864 <RE2>

A/Cross-references: GB:M86376; NID:g207459; PIDN:AAA42272.1; PID:g207462  
 C/Genetics:  
 A/Intons: 277/1; 292/1; 308/1; 339/1; 359/1; 419/1; 437/1; 467/1; 484/1; 601/1; 621/1;

A/Note: the list of introns may be incomplete  
 C/Superfamily: elastin  
 C/Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxyllysine

F/1-21/Domain: signal sequence #status predicted <SIG>  
 F/22-864/Product: elastin #status predicted <MAT>  
 F/854-859/Disulfide bonds: #status predicted

Query Match 62.3%; Score 326.5; DB 1; Length 864;  
 Best Local Similarity 67.3%; Pred. No. 8.1e-17;  
 Matches 74; Conservative 5; Mismatches 16; Indels 15; Gaps 5;

QY 3 GGVPGAIPEGVPGVYFPAGLGGALGPGKPLKVPGLAGAGL 51  
 |||||  
 DB 30 GGVPGGLPGVPGVYFPAGLGGALGPGKPLKVPGLAGAGL 89  
 |||||  
 QY 52 GAGLGAFAVTFPAGLVPGVADAAAAYK-AAKAGAGLGGVPGV-GGLGV 99  
 |||||  
 DB 90 GAGLGY--ASRPGLVLPGGAGAAAAYKAAKAGAGLGGVPGVGV 137  
 |||||

## RESULT 4

S59623

tropoelastin - sheep  
 C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C/Date: 23-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
 C/Accession: S59623; A24758

R/Mauch, J.C.; Sandberg, L.B.; Roos, P.J.; Jimenez, F.; Christiano, A.M.; Deak, S.B.; BC  
 Matrix Biol. 14, 635-641, 1994  
 A/Title: Extensive alternate exon usage at the 5' end of the sheep tropoelastin gene.  
 A/Reference number: S59623  
 A/Accession: S59623

A/Status: preliminary; not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-770 <MAU>

A/Cross-references: UNIPROT:P11547  
 R/Yoon, K.; Davidson, J.M.; Boyd, C.; May, M.; LaValle, P.; Ornstein-Goldstein, N.; Smir

Arch. Biochem. Biophys. 241, 684-691, 1985  
 A/Title: Analysis of the 3' region of the sheep elastin gene.  
 A/Reference number: A24758; MUID:85305763; PMID:3839997

A/Accession: A24758  
 A/Molecule type: mRNA

The oxidase activity.

Cnetrics: 634/3; 653/3; 676/3; 689/3; 707/3; 716/3; 733/3

A>Introns: the list of introns is incomplete

A>Note: elastin

C:Superfamily: elastin

C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxyllysine

F:1-747/Product: elastin precursor, splice form a #status predicted <EPA>

F:1-225,260-747/Product: elastin precursor, splice form c #status predicted <ERC>

F:1-225,240-747/Product: elastin precursor, splice form b #status predicted <SIG>

F:1-65/Domain: signal sequence #status predicted <MAT>

F:127-747/Product: elastin #status predicted <MAT>

P:105,109,252,271,275,324,327,400,404,407,445,448,489,493,544,548,552,606,609,645,649,673,737-742/Isoptide bonds: #status experimental

Query Match 61.9%; Score 324.5; DB 1; Length 747;  
Best Local Similarity 68.3%; Pred. No. 1e-16;  
Matches 71; Conservative 4; Mismatches 22; Indels 7; Gaps 4;

Oy 3 GGVEGALPGGVGGVFPFGAGLGLGAGLPKPVPGSLAGAFAPVT 62  
||| |||| |  
Db GGVEGAIVPVGVPFPPGAGLGVLGPVKPKPVGSLVPELGAEHLPg-A 85  
||||| |  
63 PPGAAL--VPGGVADAAAAYK-AAKAGA---GLGVPVPGVGLGS 100  
||| |||| |  
Db PPGEFFPAGGAGAAATAAATKAAGAAGLVGSGIGTGGLGS 129  
||| |||| |

RESULT 6  
A26601  
elastin precursor - chicken (fragment)  
N:Alternate names: tropoelastin  
C:Species: Gallus gallus (Chicken)  
C:Date: 05-Oct-1998 #sequence revision 26-Jul-1996 #text change 09-Jul-2004  
C:Accession: A26601; A30795; A27264  
R:Bressan, G.M.; Argos, P.; Stanley, K.K.  
Biochemistry 26, 1497-1503, 1987  
A>Title: Repeating structure of chick tropoelastin revealed by complementary DNA cloning  
A:Reference number: A26601; MUID:87242320; PMID:3593675  
A:Accession: A26601  
A:Molecule type: mRNA  
A:Residues: 1-212,237-524,535-784 <BR2>  
A:Cross-references: UNIPROT:P07916; GB:M15889; NID:g212803; PIDN:AAA49108.1; PID:g21280  
R:Baule, V.J.; Foster, J.A.  
Biochem. Biophys. Res. Commun. 154, 1054-1060, 1988  
A>Title: Multiple chick tropoelastin mRNAs.  
A:Reference number: A30795; MUID:88309083; PMID:2841924  
A:Accession: A30795  
A:Molecule type: mRNA  
A:Residues: 85-784 <BRU>  
A:Cross-references: GB:M12880; NID:g212741; PIDN:AAA49082.1; PID:g212742  
R:Tokimatsu, I.; Tajima, S.; Nishikawa, T.; Tajima, M.; Fukasawa, T.  
Arch. Biochem. Biophys. 256, 455-461, 1987  
A>Title: Sequence analysis of elastin cDNA from chick aorta and tissue-specific transcr  
A:Reference number: A27264; MUID:87297534; PMID:3502711  
A:Accession: A27264  
A:Molecule type: mRNA  
A:Residues: 491-559,'G','571-604','A','606-643','A','645-687','R','689-700','R','702-784 <TOK>  
A:Cross-references: GB:M18633; NID:g211742; PIDN:AAA48761.1; PID:g211743  
C:Superfamily: elastin  
C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine  
F:1-74/Domain: signal sequence (Fragment) #status predicted <SIG>  
F:25-212,237-554,535-784/Product: elastin #status predicted <MAT>  
F:773-779/Dissulfide bonds: #status predicted

Query Match 59.2%; Score 310; DB 2; Length 784;  
Best Local Similarity 61.6%; Pred. No. 1.2e-15;  
Matches 69; Conservative 3; Mismatches 18; Indels 22; Gaps 4;

Oy 3 GGVEGAIP-GGVPGGFYPPGAGLAG-----GALGPCKPLKPVGSLAG----- 48  
||| |||| |  
Db GGVEGAIFGGVPPGGGFPPGAGVGLGAGLAGAGCGKPLKPSVSLGGLGPLGLQCA 84  
||| |||| |

49 --AGLGAAGFAVTFPPGAIIVPGGVADAAAATRAAKAGACGLGVPVGGIGS 98





C:/Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
 C:/Accession: F70806  
 R:/Cole, S.T.; Brosch, R.; Parhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998  
 A:/Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A:/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A:/Reference number: A70500; NCID:9825987; PMID:9634230  
 A:/Accession: F70806  
 A:/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:/Molecule type: DNA  
 A:/Residues: 1-1901 <COL>  
 A:/Cross-references: UNIPROT:O53553; GB:AL022022; GB:AL123456; NID:93261554; PIDN:CAA1774  
 A:/Experimental source: strain H37Rv  
 C:/Genetics:  
 A:/Gene: RV3508  
 C:/Superfamily: collagen alpha 1(IV) chain

Query Match 26.0%; Score 136; DB 2; Length 1901;  
 Best Local Similarity 37.7%; Pred. No. 0.012; Mismatches 50; Indels 18; Gaps 4;  
 Matches 43; Conservative 3;

QY 3 GGVPGAIPG---GVPGVFPYAGAGLGGALGPG---KPLKVPQGLAGAGLGG 54  
 |||||  
 Db 192 GGVGAGGGGTGAGGPGGLIWGGGAGGAGGTGAGRAELLFAGAGAGAGTDDG 251  
 QY 55 LGAFPVAVTFPGA-----LVPGGVADA--AAAYQAARAGAGLGGVPVGGILG 98  
 |||||  
 Db 252 PGATGTGTGGHGGVGDGGLAPGAGAGAGGAGGAGSDGALGGTGTGTG 305

Search completed: August 10, 2005, 07:38:34  
 Job time : 25.3781 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2005, 07:17:42 ; Search time 111.94 Seconds

(without alignments)  
457,457 Million cell updates/sec

Title: US-09-743-818a-4\_COPY\_1\_100

Perfect score: 524

Sequence: 1 SMGVPGALPGVPGVFPV.....AAKAGAGLGVPGVGLGVIS 100

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	515	98.3	658	2	Q6P0L4
2	515	98.3	687	2	Q14235
3	515	98.3	711	2	Q7Z3F5
4	515	98.3	730	1	EL5_HUMAN
5	515	98.3	757	2	Q14234
6	515	98.3	757	2	Q75MUS
7	503	96.0	602	2	O15337
8	503	96.0	635	2	O15336
9	448	85.5	559	2	Q6ZUN2
10	448	85.5	687	2	Q7Z3I6
11	438	83.6	643	2	Q8NB14
12	377	71.9	860	1	EL5_MOUSE
13	377	71.9	860	1	Q8C9L8
14	375.5	71.7	472	2	Q8N2G0
15	351	67.0	570	2	Q6ZWC6
16	326.5	62.3	864	1	EL5_RAT
17	324.5	61.9	747	1	EL5_BOVIN
18	313	59.7	750	1	Q9BDZ0
19	310	59.2	752	1	EL5_CHICK
20	283	54.0	810	2	Q9ES29
21	245.5	46.9	650	2	Q28099
22	245.5	46.9	666	2	Q28096
23	245.5	46.9	679	2	Q28097
24	245.5	46.9	707	2	Q28098
25	171.5	32.7	258	2	Q9UMF5
26	166.5	31.8	524	2	Q8I701
27	166	30.2	1884	2	Q9NHM2
28	158.5	30.2	626	2	Q9NHM1
29	158.5	30.2	871	2	Q44358
30	158.5	30.2	2249	2	Q9NHM4
31	157.5	30.1	717	2	Q6MT66

32	156	29.8	1002	2	Q9BIU8	Q9BIU8
33	155.5	29.7	907	2	Q44359	Q44359
34	155	29.6	563	2	Q6J6N0	Q6J6N0
35	154.5	29.5	651	2	Q9BIU9	Q9BIU9
36	152.5	29.1	441	2	Q93YR3	Q93YR3
37	151.5	28.9	905	2	Q8MW55	Q8MW55
38	148	28.2	158	2	Q9SA11	Q9SA11
39	148	28.2	783	2	Q9XA11	Q9XA11
40	146.5	28.0	212	2	Q23018	Q23018
41	145.5	27.8	246	2	Q8ESZ4	Q8ESZ4
42	144.5	27.6	641	1	EBN1_EBV	EBN1_EBV
43	144.5	27.6	641	2	Q77TE1	Q77TE1
44	144	27.5	279	2	Q6C3I2	Q6C3I2
45	143.5	27.4	922	2	Q8MW53	Q8MW53

## ALIGNMENTS

RESULT 1  
ID Q6P0L4 PRELIMINARY; PRT; 658 AA.  
AC Q6P0L4;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE EBN protein.  
GN Name=EBN;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Eye;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Matrusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.E.,  
RA Brownstein M.J., Ueda T.B., Tohiyuki S., Carninci P., Mulhally S.J.,  
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bobak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywicki M.I., Skalska U., Smallos D.E., Schmechel A., Schein J.E.,  
RT Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Eye;  
RX Strausberg R.;  
RA Strausberg R.;  
DT Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
RL EMBL, BC65566; AM65566.1; -;  
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.  
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.  
DR InterPro; IPR001451; Hexapep\_transf.  
DR InterPro; IPR003979; Tropoelastin.  
DR PRINTS; PR01500; TROP0ELASTIN.  
DR PROSITE; PS00101; HEXAPEP\_TRANSFERSSES; UNKNOWN 1.  
SQ SSQCEHCE 658 AA; 56680 MW; 5DARC00D16A2F94E CRCA4;  
Query Match 98.3%; Score 515; DB 2; Length 658;  
Best Local Similarity 100.0%; Pred. No. 5,4e-25;  
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 3 GGVPAIPGGVPGVFPAGAGLGGALGPGCGPLKPVPGLAGAGAGAGFPAYT 62
    |||
DB 27 GGVPAIPGGVPGVFPAGAGLGGALGPGCGPLKPVPGLAGAGAGAGFPAYT 86
    |||

QY 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100
    |||
DB 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 124
    |||

RESULT 2
ID 014235 PRELIMINARY; PRT; 687 AA.
AC 014235;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Elastin.
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87289668; PubMed=3039501;
RA Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
RA Rosenbloom J., Ornstein-Goldstein N.,
RT "Structure of the 3' region of the human elastin gene: great abundance
RT of Alu repetitive sequences and few coding sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87274906; PubMed=3038460;
RA Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
RA Rosenbloom J., Ornstein-Goldstein N.,
RT "Structure of the 3' region of the human elastin gene: great abundance
RT of Alu repetitive sequences and few coding sequences.";
RL Connect. Tissue Res. 16:197-211(1987).
DR EMBL, M17282; AAC98393.1; -.
DR EMBL, M16983; AAC98393.1; JOINED.
DR EMBL, M17265; AAC98393.1; JOINED.
DR EMBL, M17266; AAC98393.1; JOINED.
DR EMBL, M17267; AAC98393.1; JOINED.
DR EMBL, M17268; AAC98393.1; JOINED.
DR EMBL, M17271; AAC98393.1; JOINED.
DR EMBL, M17272; AAC98393.1; JOINED.
DR EMBL, M17273; AAC98393.1; JOINED.
DR EMBL, M17275; AAC98393.1; JOINED.
DR EMBL, M17276; AAC98393.1; JOINED.
DR EMBL, M17277; AAC98393.1; JOINED.
DR EMBL, M17278; AAC98393.1; JOINED.
DR EMBL, M17279; AAC98393.1; JOINED.
DR EMBL, M17281; AAC98393.1; JOINED.
DR HSSP; P50099; 1ZFU.
DR GO; GO:0005578; Extracellular matrix (sensu Metazoa); NAS.
DR GO; GO:0030023; Extracellular matrix constituent conferring. . .; NAS.
DR InterPro; IPR001451; Hexapep_transf.
DR PRINTS; PRO1500; TROPOLASTIN.
DR PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
SQ SEQUENCE 687 AA; 59529 MW; 864068C4C8E9F88F CRC64;
```

```
DB 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 124
    |||

RESULT 3
ID 0723F5 PRELIMINARY; PRT; 711 AA.
AC 0723F5;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686F06102.
GN Name=DKFZp686F06102;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human fetal kidney;
RA Poustka A., Albert R., Moosmayer P., Schnupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amdt C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX537939; CDD97910.1; -.
DR InterPro; IPR001451; Hexapep_transf.
DR PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 711 AA; 61765 MW; 95B624A9B4A989B CRC64;

Query Match 98.3%; Score 515; DB 2; Length 711;
Best Local Similarity 100.0%; Pred. No. 5.8e-25;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPAIPGGVPGVFPAGAGLGGALGPGCGPLKPVPGLAGAGAGAGFPAYT 62
    |||
DB 27 GGVPAIPGGVPGVFPAGAGLGGALGPGCGPLKPVPGLAGAGAGAGFPAYT 86
    |||

QY 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100
    |||
DB 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 124
    |||

RESULT 4
ELS HUMAN STANDARD; PRT; 730 AA.
ID 015502; 014233; 014238;
AC 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Elastin precursor (Tropoelastin).
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM B).
RX MEDLINE=87289668; PubMed=3039501;
RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Peltonen L., Rosenbloom J.,
RT "Alternative splicing of human elastin mRNA indicated by sequence
RT analysis of cloned genomic and complementary DNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Skin fibroblast;
RX MEDLINE=89009960; PubMed=3171221;
RA Fazio M.J., Olsen D.R., Kaub E.A., Baldwin C.T., Indik Z.,
RA Ornstein-Goldstein N., Yeh H., Rosenbloom J., Uitto J.;
RT "Cloning of full-length elastin cDNAs from a human skin fibroblast
RT recombinant cDNA library: further elucidation of alternative splicing
RT utilizing exon-specific oligonucleotides.";
RL J. Invest. Dermatol. 91:458-464(1988).
RN [3]
```

RP SEQUENCE OF 164-724 FROM N.A. (ISOFORM B).

RC TISSUE=Placenta; PubMed=2831431;  
 RX MEDLINE=88156138; PubMed=2831431;  
 RA Fazio M.J., Olsen D.R., Kuivanen H., Chu M.L., Davidson J.M.,  
 Rosenbloom J., Uitto J.;  
 RT "Isolation and characterization of human elastin cDNAs, and age-  
 associated variation in elastin gene expression in cultured skin  
 fibroblasts.";  
 RL Lab. Invest. 58:270-277 (1988).  
 RN [4]  
 RP SEQUENCE OF 603-730 FROM N.A.  
 RC TISSUE=Hipocampus, and Placenta;  
 RX MEDLINE=9629139; PubMed=8698988; DOI=10.1016/S0092-8674(00)80077-X;  
 RA Frangiskakis J.M., Ewert A.K., Morris C.A., Mervis C.B., Bertrand J.,  
 Robinson B.F., Klein B.P., Ensing G.J., Everett U.A., Green E.D.,  
 Proeschel C., Gutowski N.J., Noble M., Atkinson D.L., Odelberg S.J.,  
 Keating M.T.;  
 RT "Lim-kinase1 hemizyosity implicated in impaired visuospatial  
 constructive cognition.";  
 RL Cell 86:59-69 (1996).  
 RN [5]  
 RP INVOLVEMENT IN CUTIS LAXA.  
 RX MEDLINE=99091639; PubMed=9873040; DOI=10.1074/jbc.274.2.981;  
 RA Zhang M.-C., He L., Giro M., Yong S.L., Tiller G.E., Davidson J.M.;  
 RT "Cutis laxa arising from frameshift mutations in exon 30 of the  
 elastin gene (ELN).";  
 RL J. Biol. Chem. 274:981-986 (1999).  
 RN [6]  
 RP INVOLVEMENT IN SVAS.  
 RX PubMed=10942104;  
 RA Urban Z., Michels V.V., Thibodeau S.N., Davis E.C., Bonnefont J.-P.,  
 Munich A., Syskens B., Gewillig M., Devriendt K., Boyd C.D.;  
 RT "Isolated supravalvular aortic stenosis: functional haploinsufficiency  
 of the elastin gene as a result of nonsense-mediated decay.";  
 RL Hum. Genet. 106:577-588 (2000).  
 CC -1- FUNCTION: Major structural protein of tissues such as aorta and  
 nuchal ligament, which must expand rapidly and recover completely.  
 CC -1- SUBUNIT: The polymeric elastin chains are cross-linked together  
 CC into an extensible 3D network.  
 CC -1- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=1;  
 CC IsoId=P15502-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=P15502-2; Sequence=VSP\_004243;  
 CC -1- PTM: The crosslinks are made of deaminated lys.  
 CC -1- DISEASE: Defects in ELN are a cause of autosomal dominant cutis  
 CC laxa [MIM:123700]. Cutis laxa is a rare connective tissue disorder  
 CC characterized by loose, hyperextensible skin with decreased  
 CC resilience and elasticity leading to a premature aged appearance.  
 CC The skin changes are often accompanied by extracutaneous  
 CC manifestations, including pulmonary emphysema, bladder  
 CC diverticula, pulmonary artery stenosis and pyloric stenosis.  
 CC -1- DISEASE: Haploinsufficiency of ELN may be the cause of certain  
 CC cardiovascular and musculo-skeletal abnormalities observed in  
 CC Williams-Beuren syndrome (WBS) [MIM:194050]. WBS is a rare  
 CC developmental disorder and a contiguous gene deletion syndrome  
 CC involving genes from chromosome band 7q11.23.  
 CC -1- DISEASE: Defects in ELN are the cause of supravalvular aortic  
 CC stenosis (SVAS) [MIM:185500]. SVAS is a congenital narrowing of  
 CC the ascending aorta which can occur sporadically, as an autosomal  
 CC dominant condition, or as one component of Williams-Beuren  
 CC syndrome.  
 CC -----  
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CC -----

DR EMBL: M17282; AAC98394.1; -;  
 DR EMBL: M16983; AAC98394.1; JOINED.  
 DR EMBL: M17265; AAC98394.1; JOINED.  
 DR EMBL: M17266; AAC98394.1; JOINED.  
 DR EMBL: M17267; AAC98394.1; JOINED.  
 DR EMBL: M17268; AAC98394.1; JOINED.  
 DR EMBL: M17270; AAC98394.1; JOINED.  
 DR EMBL: M17271; AAC98394.1; JOINED.  
 DR EMBL: M17272; AAC98394.1; JOINED.  
 DR EMBL: M17273; AAC98394.1; JOINED.  
 DR EMBL: M17275; AAC98394.1; JOINED.  
 DR EMBL: M17276; AAC98394.1; JOINED.  
 DR EMBL: M17277; AAC98394.1; JOINED.  
 DR EMBL: M17278; AAC98394.1; JOINED.  
 DR EMBL: M17279; AAC98394.1; JOINED.  
 DR EMBL: M17280; AAC98394.1; JOINED.  
 DR EMBL: M17281; AAC98394.1; JOINED.  
 DR EMBL: M36860; AAA52382.1; -;  
 DR EMBL: M24782; AAA53190.1; -;  
 DR EMBL: U62292; AAB17544.1; -;  
 DR EMBL: X15603; CAA33627.1; -;  
 DR PIR: A32707; EAHU.  
 DR HSSP: P50099; 1ZFU.  
 DR Genew: HGNC:3327; ELN.  
 DR MIM: 130160; -;  
 DR MIM: 123700; -;  
 DR MIM: 194050; -;  
 DR MIM: 185500; -;  
 DR CO: GO:0005578; C:extracellular matrix; TAS.  
 DR CO: GO:0005615; C:extracellular space; TAS.  
 DR CO: GO:0005201; F:extracellular matrix structural constituent; TAS.  
 DR CO: GO:0008283; P:cell proliferation; TAS.  
 DR CO: GO:0008015; P:circulation; TAS.  
 DR CO: GO:0009887; P:organogenesis; TAS.  
 DR CO: GO:0007585; P:respiratory gaseous exchange; TAS.  
 DR InterPro: IP003979; Tropoelastin.  
 DR PRINTS: PR01500; TROP0ELASTIN.  
 KW Alternative splicing; Repeat; Signal; Structural protein;  
 KW Williams-Beuren syndrome.  
 FT CHAIN 1 26  
 FT SIGNAL 1 26  
 FT DISUPID 720 725  
 FT VARSPIC 472 477  
 FT FTId=VSP\_004243.  
 FT FTId=VSP\_004243.  
 SQ SEQUENCE 730 AA; 63260 MW; AB06D15BA567AE46 CRC64;  
 Query Match 98.3%; Score 515; DB 1; Length 730;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-25;  
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GGVGAIIPGVPGVFPVPGAGLGGALGPGKPLKPVPGLAGAGLGAAPPVAT 62  
 DB 27 GGVGAIIPGVPGVFPVPGAGLGGALGPGKPLKPVPGLAGAGLGAAPPVAT 86  
 QY 63 FPGALVPGVADAAAYKAKAKAGAGCGVGVGGLGVS 100  
 DB 87 FPGALVPGVADAAAYKAKAKAGAGCGVGVGGLGVS 124  
 RESULT 5  
 Q14234 PRELIMINARY; PRT; 757 AA.  
 ID Q14234;  
 AC Q14234;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DN Elastin.  
 GN Name=ELN;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxId=9606;

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RN      (1)
RP      SEQUENCE FROM N.A.
RX      MEDLINE=87289668; PubMed=3039501;
RA      Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
RA      Rosenbloom J.C., Peltonen L., Rosenbloom J.;
RT      "Alternative splicing of human elastin mRNA indicated by sequence
RT      analysis of cloned genomic and complementary DNA.";
RL      Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=87274906; PubMed=3038460;
RA      Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
RA      Rosenbloom J., Ornstein-Goldstein N.;
RT      "Structure of the 3' region of the human elastin gene: great abundance
RT      of Alu repetitive sequences and few coding sequences.";
RL      Connect. Tissue Res. 16:197-211(1987).
DR      EMBL; M17282; AAC98395.1; -.
DR      EMBL; M16983; AAC98395.1; JOINED.
DR      EMBL; M17265; AAC98395.1; JOINED.
DR      EMBL; M17266; AAC98395.1; JOINED.
DR      EMBL; M17267; AAC98395.1; JOINED.
DR      EMBL; M17268; AAC98395.1; JOINED.
DR      EMBL; M17270; AAC98395.1; JOINED.
DR      EMBL; M17271; AAC98395.1; JOINED.
DR      EMBL; M17272; AAC98395.1; JOINED.
DR      EMBL; M17273; AAC98395.1; JOINED.
DR      EMBL; M17274; AAC98395.1; JOINED.
DR      EMBL; M17275; AAC98395.1; JOINED.
DR      EMBL; M17276; AAC98395.1; JOINED.
DR      EMBL; M17277; AAC98395.1; JOINED.
DR      EMBL; M17278; AAC98395.1; JOINED.
DR      EMBL; M17279; AAC98395.1; JOINED.
DR      EMBL; M17280; AAC98395.1; JOINED.
DR      EMBL; M17281; AAC98395.1; JOINED.
DR      GO; GO:0005578; C:extracellular matrix (sensu Metazoa); NAS.
DR      GO; GO:0030023; F:extracellular matrix constituent conferring. . .; NAS.
DR      InterPro; IPR001451; Hexapep.transf.
DR      PRINTS; PR01500; TROPOELASTIN.
DR      PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
SQ      SEQUENCE 757 AA; 66136 MW; 23B7F5B8AF85CA8 CRC64;

Query Match          98.3%; Score 515; DB 2; Length 757;
Best Local Similarity 100.0%; Pred. No. 6e-25;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GGVPGAI PGGVGVPYPPAGLGGALGGGALPGGKPLKVPVPGLAGAGLAGAPPAVT 62
        |||||
DB      27 GGVPGAI PGGVGVPYPPAGLGGALGGGALPGGKPLKVPVPGLAGAGLAGAPPAVT 86
        |||||

QY      63 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGLGVS 100
        |||||
DB      87 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGLGVS 124
        |||||

RESULT 6
ID      075MUS          PRELIMINARY;      PRT;      757 AA.
AC      075MUS;
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE      Hypo-2004 (TrEMBLrel. 27, Last annotation update)
DE      Hypothetical protein ELN.
GN      Name=ELN;
OS      Homo sapiens (human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC      NCBI_Taxid=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
RA      Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA      Wagner-McPherson C., Layman D., Maa J., Jaeger S., Walker R.,

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RA      Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA      Fowell G.A., Delehaunty K.D., Miner T.L., Nash W.B., Cordes M., Du H.,
RA      Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA      Vanhurn A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA      Ozerovsk P., Bellick L., Scott K., Holmes A., Harkins R., Harris A.,
RA      Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA      Kozlowski-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RA      Tin-Lowell A.M., Abbott A., Mink P., Maupin R., Strommatt C.,
RA      Latreille P., Miller N., Johnson D., Murray J., Moessner J.P.,
RA      Wendt M.C., Yang S.P., Schultz B.R., Wallis J.W., Spiech J.,
RA      Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
RA      Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA      Clifton S.W., Chisoe S.L., Marra M.A., Raymond C., Haugen E.,
RA      Gillett W., Zhou Y., James R., Phelps K., Iadamoto S., Bubb K.,
RA      Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
RA      Baertsch R.A., Brent M.R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
RA      Bailey J.A., Portnoy M.E., Torrents D., Chikwalla A.T., Gish W.R.,
RA      Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA      Waterston R.H., Wilson R.K.;
RT      "The DNA sequence of human chromosome 7.";
RL      Nature 424:157-164(2003).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Waterston R.;
RT      Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RA      Wilson R.;
RL      Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AC005056; AAS07435.1; -.
DR      GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR      GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR      InterPro; IPR001451; Hexapep.transf.
DR      PRINTS; PR01500; TROPOELASTIN.
DR      PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
DR      Hypothetical protein.
SQ      SEQUENCE 757 AA; 66106 MW; 2B24F95D8360738 CRC64;

Query Match          98.3%; Score 515; DB 2; Length 757;
Best Local Similarity 100.0%; Pred. No. 6e-25;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GGVPGAI PGGVGVPYPPAGLGGALGGGALPGGKPLKVPVPGLAGAGLAGAPPAVT 62
        |||||
DB      27 GGVPGAI PGGVGVPYPPAGLGGALGGGALPGGKPLKVPVPGLAGAGLAGAPPAVT 86
        |||||

QY      63 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGLGVS 100
        |||||
DB      87 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGLGVS 124
        |||||

RESULT 7
ID      015337          PRELIMINARY;      PRT;      602 AA.
AC      015337;
DT      01-JAN-1998 (TrEMBLrel. 05, Created)
DT      01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Elastin (Fragment).
OS      Homo sapiens (human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC      NCBI_Taxid=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=9758574; PubMed=9215670; DOI=10.1093/hmg/6.7.1021;
RA      Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,
RA      Morris C.A., Keating M.T.;
RT      "Elastin point mutations cause an obstructive vascular disease,
RT      supravalvular aortic stenosis.";
RL      Hum. Mol. Genet. 6:1021-1028(1997).
DR      EMBL; U93037; AAB65620.1; -.

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DR EMBL: U93034; AAB65620.1; JOINED.  
DR EMBL: U93035; AAB65620.1; JOINED.  
DR EMBL: U93036; AAB65620.1; JOINED.  
DR GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.  
DR GO: GO:0005201; F:extracellular matrix structural constituent; IEA.  
DR InterPro: IPR001451; Hexaped\_transf.  
DR InterPro: IPR003979; troponelastin.  
DR PRINTS: PRO1500; TROPOELASTIN.  
DR PROSITE: PS00101; HEXAPEP\_TRANSFERRASES; UNKNOWN\_1.  
FT NON TER 1  
FT NON TER 602  
SQ SEQUENCE 602 AA; 51807 MW; 53B5B9A71EF04807 CRC64;

Query Match 96.0%; Score 503; DB 2; Length 602;  
Best Local Similarity 100.0%; Pred. No. 2.9e-24;  
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPQAIPEGVPGVFPYPPAGLGGALGGGKPLKVPVPGLAGAGLGAFFPAVTFP 64  
DB 1 VPQAIPEGVPGVFPYPPAGLGGALGGGKPLKVPVPGLAGAGLGAFFPAVTFP 60

QY 65 GALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100  
DB 61 GALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 96

RESULT 8  
O15336 PRELIMINARY; PRT; 635 AA.

ID O15336;  
AC O15336;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JUN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Elasin (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxID=9606;

RN  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9735874; PubMed=9215670; DOI=10.1093/hmg/6.7.1021;  
RI D.Y. Toland A.B., Boak B.B., Atkinson D.L., Ensing G.J.,  
RA Morris C.A., Keating M.T.  
RT "Elastin point mutations cause an obstructive vascular disease,  
supravalvular aortic stenosis."  
RL Hum. Mol. Genet. 6:1021-1028(1997).  
DR EMBL: U93037; AAB65621.1; -.  
DR EMBL: U93034; AAB65621.1; JOINED.  
DR EMBL: U93035; AAB65621.1; JOINED.  
DR GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.  
DR GO: GO:0005201; F:extracellular matrix structural constituent; IEA.  
DR InterPro: IPR001451; Hexaped\_transf.  
DR InterPro: IPR003979; troponelastin.  
DR PRINTS: PRO1500; TROPOELASTIN.  
DR PROSITE: PS00101; HEXAPEP\_TRANSFERRASES; UNKNOWN\_1.  
FT NON TER 1  
FT NON TER 635  
SQ SEQUENCE 635 AA; 55279 MW; 72950C364127B2A4 CRC64;

Query Match 96.0%; Score 503; DB 2; Length 635;  
Best Local Similarity 100.0%; Pred. No. 3e-24;  
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPQAIPEGVPGVFPYPPAGLGGALGGGKPLKVPVPGLAGAGLGAFFPAVTFP 64  
DB 1 VPQAIPEGVPGVFPYPPAGLGGALGGGKPLKVPVPGLAGAGLGAFFPAVTFP 60

QY 65 GALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100  
DB 61 GALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 96

RESULT 9  
O6ZUN2 PRELIMINARY; PRT; 559 AA.

ID O6ZUN2;  
AC O6ZUN2;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein FLJ43523.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxID=9606;  
RN  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,  
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,  
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,  
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,  
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuna M.,  
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,  
RA Sugano S., Nagahari K., Masuno Y., Nagai K., Isogai T.,  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AK125511; BAC6188.1; -.  
DR GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.  
DR GO: GO:0005201; F:extracellular matrix structural constituent; IEA.  
DR InterPro: IPR003979; troponelastin.  
DR PRINTS: PRO1500; TROPOELASTIN.  
DR PROSITE: PS00101; HEXAPEP\_TRANSFERRASES; UNKNOWN\_1.  
SQ SEQUENCE 559 AA; 53787 MW; 20938FEEC5492A01 CRC64;

Query Match 85.5%; Score 448; DB 2; Length 559;  
Best Local Similarity 89.8%; Pred. No. 7.8e-21;  
Matches 88; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 GGVPAIPEGVPGVFPYPPAGLGGALGGGKPLKVPVPGLAGAGLGAFFPAVTFP 62  
DB 27 GGVPAIPEGVPGVFPYPPAGLGGALGGGKPLKVPVPGLAGAGLGAFFPAVTFP 76

QY 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100  
DB 77 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 114

RESULT 10  
O7Z316 PRELIMINARY; PRT; 687 AA.

ID O7Z316;  
AC O7Z316;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein DKFZ686021208 (Fragment).  
GN Name=DKFZ686021208;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxID=9606;

RN  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RA Lauber J., Bahr A., Mewes H.W., Well B., Amid C., Osanger A., Fobo G.,  
RA Han W., Wiemann S.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BX538199; CAD98065.1; -.  
DR InterPro: IPR001451; Hexaped\_transf.  
DR PROSITE: PS00101; HEXAPEP\_TRANSFERRASES; UNKNOWN\_1.  
KM Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 687 AA; 59847 MW; 79232A191DC1F10F CRC64;

Query Match 85.5%; Score 448; DB 2; Length 687;  
Best Local Similarity 89.8%; Pred. No. 9.1e-21;  
Matches 88; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

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QY 3 GGVPGAIPEGVPGVFPYFGAGLGGALGPGKRLKPVPGLAGAGLGAAGFPAVT 62
    |||||
DB 37 GGVPGAIPEGVPGVFPY-----ALGPGKRLKVPVPGLAGAGLGAAGFPAVT 86
    |||||

QY 63 FPGALVPGGVADAAAAYKAAKAGAGLGVPGVGGGAGS 100
    |||||
DB 87 FPGALVPGGVADAAAAYKAAKAGAGLGVPGVGGGAGS 124
    |||||

RESULT 11
Q8NB14 PRELIMINARY; PRT; 643 AA.
AC Q8NB14;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein F58C0254.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCB1_TaxID=9606;
RX [1]
RP SEQUENCE FROM N.A.
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayaishi K., Ishii S.,
RA Saito K., Yamamoto J., Makamatsu A., Nagai T., Nakamura Y.,
RA Nagahara K., Sugano S., Isogai T.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075554; BAC11696.1; -.
DR HSSP; P50099; 1ZFU.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0005201; P:extracellular matrix structural constituent, IEA.
DR InterPro; IPR001451; Hexadep.transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROP0ELASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSPERASES; UNKNOWN 1.
DR SEQUENCE 643 AA; 55629 MW; PFC042617E72A69 CRC64;

Query Match
Best local Similarity 83.6%; Score 438; DB 2; Length 643;
Matches 86; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

QY 3 GGVPGAIPEGVPGVFPYFGAGLGGALGPGKRLKPVPGLAGAGLGAAGFPAVT 62
    |||||
DB 27 GGVPGAIPEGVPGVFPYFGAGLGGALGPGKRLK-----GLGAPPAVT 74
    |||||

QY 63 FPGALVPGGVADAAAAYKAAKAGAGLGVPGVGGGAGS 100
    |||||
DB 75 FPGALVPGGVADAAAAYKAAKAGAGLGVPGVGGGAGS 112
    |||||

RESULT 12
EUS_MOUSE
ID EUS_MOUSE STANDARD; PRT; 860 AA.
AC P54320;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Elastin precursor (Tropoelastin).
GN Name=Eln;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCB1_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BALB/c; TISSUE=Lung;
RA MEDLINE=95130069; PubMed=7829060;
RA Wyder K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
RT "Use of an intron polymorphism to localize the tropoelastin gene to
RT mouse chromosome 5 in a region of linkage conservation with human
RT chromosome 7.";
RL Genomics 23:125-131(1994).
CC -I- FUNCTION: Major structural protein of tissues such as aorta and

```

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CC nuchal ligament, which must expand rapidly and recover completely.
CC -I- SUBUNIT: The polymeric elastin chains are cross-linked together
CC into an extensible 3D network.
CC -I- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
CC -I- PTM: The crosslinks are made of deaminated Lys.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; U08210; AAA80155.1; -.
CC PIR; A55721; EAMS.
CC MGI; MGI:95317; Rln.
CC InterPro; IPR003979; tropoelastin.
CC PRINTS; PR01500; TROP0ELASTIN.
CC Repeat; Signal; Structural protein.
CC FT SIGNAL 1 27 Potential.
CC FT CHAIN 28 860 Elastin.
CC FT DISULFID 850 855 By similarity.
CC FT SEQUENCE 860 AA; 71955 MW; 0C0B53AE1EDD7F1 CRC64;

Query Match
Best local Similarity 71.9%; Score 377; DB 1; Length 860;
Matches 82; Conservative 4; Mismatches 11; Indels 16; Gaps 5;

QY 3 GGVPGAIPEGVPGVFPYFGAGLGGALGPGKRLK-----VPGLAGAG 50
    |||||
DB 32 GAVPGGLPEGVPGVFPYFGAGLGGAGLGGKRLKPGAGLGTGAGPGGIGGAG 91
    |||||

QY 51 LGAGLGAFFAVTFP--GALVPGGVADAAAAYK-AAKAGAGLGVPGV--GGLGV 99
    |||||
DB 92 PAGLGAFFAVTFPAGLALVPGGAAGAAAYKAAKAGAGLGGVGGVPGVGV 144
    |||||

RESULT 13
Q8C9L8 PRELIMINARY; PRT; 860 AA.
AC Q8C9L8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
DE library, clone:A630042119 product:elastin, full insert sequence
DE (Elaetin).
GN Name=Eln;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCB1_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Thymus;
RA MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carinci P., Hayaishi K. Y.;
RT "High-efficiency full-length cDNA cloning.";
RT Meth. Enzymol. 303:19-44(1999).
RX [2]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Thymus;
RA MEDLINE=21085660; PubMed=11217651; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
RX [3]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Thymus;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of

```

RT 60 770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 Kono H., Akiyama J., Nishi K., Kitanai T., Tashiro H., Itoh M.,  
 "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT Prepare full-length cDNA libraries for rapid discovery of new genes."  
 RL Genome Res. 10:1617-1630(2000).  
 [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 Kono H., Akiyama J., Nishi K., Kitanai T., Tashiro H., Itoh M.,  
 Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 Fujisake S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,  
 Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai U.,  
 Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
 "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer."  
 RL Genome Res. 10:1757-1771(2000).  
 [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
 Kurihara K., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,  
 Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
 "Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases."  
 [7]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahy J., Hailton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Blakesley A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,  
 Rodriguez M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,  
 Krzywicki M.I., Marra M.A.,  
 "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [8]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RA Strausberg R.,  
 "Submitted (APR-2003) to the EMBL/GenBank/DBJ databases."  
 RX EMBL: AK041860; BAC31084.1; -.  
 DR EMBL: BC051649; AA51649.1; -.  
 DR MGD: MGI:95317; Eln.  
 DR GO: GO:0007519; P:myogenesis; IMP.

DR GO: GO:0030833; P:regulation of actin filament polymerization; IMP.  
 DR GO: GO:0043149; P:stress fiber formation; IMP.  
 DR InterPro: IPR003979; tropoelastin.  
 DR PRINTS: PRO1500; TROPELASTIN.  
 SQ SEQUENCE 860 AA; 71938 MW; 7C340F2FFDC92E5 CRC64;  
 Query Match 71.9%; Score 377; DB 2; Length 860;  
 Best Local Similarity 72.6%; Pred. No. 3.1e-16;  
 Matches 82; Conservative 4; Mismatches 11; Indels 16; Gaps 5;  
 QY 3 GGVPGAIIPGVPGVPGVPGAGLAL--GGGALPGGKPLKP-----VGGLAGAG 50  
 Db 32 GAVPGGLPGVPGVPGVYPPAGIGIGLGGGGGALPGGKPPRGAGLGTFGAGPGGLGAG 91  
 QY 51 LGAGLGAFFPVTP--GALVPGGVADAAAAYK-AAAGAGLGGVPGV--GGAGV 99  
 Db 92 PGAGLGAFFAGTTPPGAGALVPGAGAGAAAAYKAAAGAGLGGVPGVGV 144  
 RESULT 14  
 Q8N2G0 PRELIMINARY; PRT; 472 AA.  
 ID Q8N2G0;  
 AC Q8N2G0;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein PSEC0191.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole embryo;  
 RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,  
 Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,  
 Negahari K., Sugano S., Isogai T.,  
 "Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases."  
 RX EMBL: AK075494; BAC11651.1; -.  
 DR GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.  
 DR GO: GO:0005201; F:extracellular matrix structural constituent; IEA.  
 DR InterPro: IPR001451; Hexadep. transf.  
 DR InterPro: IPR003979; tropoelastin.  
 DR PRINTS: PRO1500; TROPELASTIN.  
 DR POSITE; PS00101; HEXADEP\_TRANSFERRASES; UNKNOWN\_1.  
 FT NON TER 472 472  
 SQ SEQUENCE 472 AA; 42265 MW; 8D7A0F3A9BF971F3 CRC64;  
 Query Match 71.7%; Score 375.5; DB 2; Length 472;  
 Best Local Similarity 79.4%; Pred. No. 2.5e-16;  
 Matches 77; Conservative 1; Mismatches 18; Indels 1; Gaps 1;  
 QY 3 GGVPGAIIPGVPGVPGVPGAGLALGGGALPGGKPLKPVGGLAGAGLGAAPPVAT 62  
 Db 27 GGVPGAIIPGVPGVPGVPGAGLALGGGALPGGKPLKPVGGLAGAGLGAAGLGGV 86  
 QY 63 FPGALVPGG-VADAAAAYKAAAGAGLGGVPGVGG 98  
 Db 87 IPGAVGAGPAAAAAAAKAAKYGAAAGLVPGGPRFG 123  
 RESULT 15  
 Q6ZM06 PRELIMINARY; PRT; 570 AA.  
 ID Q6ZM06;  
 AC Q6ZM06;  
 DT 05-JUN-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein FLJ16246.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;

RN [1]  
RP SEQUENCE FROM N.A.  
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,  
RA Wakebe H., Ono T., Hashigaki H., Matanabe T., Ozaki K., Sugiyama T.,  
RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,  
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,  
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,  
RA Wagaetsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,  
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,  
RA Masuno Y., Nagai K., Isogai T.,  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK122731; BAC85506.1; -  
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.  
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.  
DR InterPro; IPR003979; tropoelastin.  
DR InterPro; IPR001451; Hexapep\_transf.  
DR PRINTS; PR01500; TROPELASTIN.  
DR PROSITE; PS00101; HEXAPEP\_TRANSFERASES; UNKNOWN\_1.  
SQ SEQUENCE 570 AA; 48941 MW; 3117B028D06D4F7B CRC64;

Query Match 67.0%; Score 351; DB 2; Length 570;  
Best Local Similarity 57.4%; Pred. No. 9.9e-15;  
Matches 81; Conservative 2; Mismatches 12; Indels 46; Gaps 5;  
QY 3 GGVPGAI PGVPGVFPY PGAGL GAGL GPGKPLK PVP GGLAGL GAGL-GA FPAV 61  
Db 27 GGVPGAI PGVPGVFPY PGAGL GAGL GPGKPLK PVP GGLAGL GAGL GAGVGA FAGI 86  
QY 62 TRPG-----ALVPGVAD-----AAAY 79  
Db 87 --PGVPPFGAPQPGVPLGYPIKAPKLPGYPGGVAGAGAKAGYPTGTGVPQAAAAAAR 144  
QY 80 KAAKAGAGLGV-PGYGGLGV 99  
Db 145 AAARFGAGAGVLPVGGAGV 165

Search completed: August 10, 2005, 07:37:41  
Job time : 113.94 secs

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OM protein - protein search, using .sw model

Run on: August 10, 2005, 07:16:57 ; Search time 120.095 Seconds  
(without alignments)  
325.267 Million cell updates/sec

Title:	US-09-743-818A-4_COPY_500_600
Perfect score:	501
Sequence:	1 VAAAKSAKVAAKAQLRAA.....QHLPSTPSSPRVPGALAAK 101

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Searched:      2105692 begs, 386760381 residues
Total number of hits satisfying chosen parameters: 21056922
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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%
	Listing first	45 summaries

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1: Geneseqp186c04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2004s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	501	100.0	730	2	AAM46315	AaW46335 Human elia
2	501	100.0	731	3	AA659068	AAy659068 Amino aci
3	501	100.0	731	4	AAB66657	Aab66657 Human elia
4	501	100.0	731	6	ABU08725	ABu08725 Human elia
5	501	100.0	731	7	ADU96420	AdU96420 Human elia
6	501	100.0	733	2	AAS65653	AArs65653 Synthetic
7	501	100.0	733	2	AAAY01301	AAy01301 Amino aci
8	501	100.0	757	7	ABG75223	ABg75223 Human tro
9	501	100.0	757	7	ADP65160	ADp65160 Human elia
10	424	84.6	216	2	AAAY01310	AAy01310 Human tro
11	308	61.5	200	2	AAAY01305	AAy01305 Human tro
12	304.5	60.8	617	7	ADB64761	ADb64761 Human pro
13	304.5	60.8	660	2	ADMY01303	ADm01303 Human tro
14	304.5	60.8	663	7	ADM03792	ADm03792 Human pro
15	304.5	60.8	692	7	ADe40134	ADe40134 Human NOV
16	304.5	60.8	698	2	AAAY01302	AAy01302 Human tro
17	304.5	60.8	698	2	AAAY69069	AAy69069 Amino aci
18	304.5	60.8	712	3	AAB08630	AaB08630 Amino aci
19	304.5	60.8	730	3	AAB08631	AaB08631 Fusion pr
20	304.5	60.8	730	5	AAO17360	AaO17360 Human elia
21	304.5	60.8	730	8	ADQ19747	ADq19747 Human sof
22	304.5	60.8	870	7	ADBO8527	ADe08527 Novel
23	303.5	60.6	570	8	ADQ65871	ADq65871 Novel hum
24	301.5	60.0	711	7	ADe40132	ADe40132 Human NOV
25	300.5	60.0	472	4	AAB86422	AaB86422 Human mem

## ALIGNMENTS

26	266	53.1	571	3	AA69071	Aa69071	Antio acti
27	249.5	49.8	864	7	AD56670	Ad56670	Rat Prote
28	227.5	45.4	183	2	AA01311	Aa01311	Human ttr
29	227.5	45.4	183	3	AA69138	Aa69138	Human ttr
30	191	38.1	171	3	AA69137	Aa69137	Human ttr
31	174	34.7	34	2	AA01308	Aa01308	Human ttr
32	170	33.9	34	2	AA01309	Aa01309	Human ttr
33	159	31.7	34	1	AA671455	Aa671455	Sequence
34	159	31.7	217	2	AA80347	Aa80347	Protein p
35	159	31.7	281	2	AA49736	Aa49736	Protein p
36	158	31.5	223	2	AA80348	Aa80348	Protein p
37	158	31.5	287	2	AA49737	Aa49737	Protein p
38	155	30.9	877	2	AA80335	Aa80335	Protein p
39	155	30.9	877	2	AA49722	Aa49722	Protein p
40	154.5	30.8	235	2	AA80349	Aa80349	Protein p
41	154	30.7	246	8	ADR70475	Ad70475	Silk-elasi
42	154	30.7	246	8	ADR70476	Ad70476	Silk-elasi
43	154	30.7	246	8	ADR70474	Ad70474	Silk-elasi
44	154	30.7	884	2	AA80341	Aa80341	Protein p
45	154	30.7	884	2	AA09213	Aa09213	SHLP8K pc

## RESULT 1

ID	AA046315	standard; protein; 730 AA.
XX		
AC	AA046315;	
XX		
DT	23-JUL-1998	(first entry)
XX		
DE	Human elastin containing non-natural polypeptide MFU-1 sequence.	
XX		
KW	MFU-1; minimal functional unit; elastin; human; fibrous protein;	
KW	beta-sheet; coating; wound dressing.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Protein	374..499
FT		/note="MFU-1 polypeptide"
XX		
PN	WC0805685-A2.	
XX		
PD	12-FEB-1998.	
XX		
PF	07-AUG-1997;	97WC-CA000560.
XX		
PR	07-AUG-1996;	96US-0023552P.
PR	07-AUG-1997;	97US-00911364.
XX		
PA	(PROT-) PROTEIN SPECIALTIES LTD.	
PA	(HOSP-) HOSPITAL FOR SICK CHILDREN.	
XX		
PI	Rothstein A, Keeley FW, Rothstein SJ;	
XX		
DR	WPI; 1998-145551/13.	
XX		
PT	New non-natural polypeptide with multiple beta-sheet, beta-turn	
PT	structures - particularly based on human elastin, useful for coating	
PT	prostheses, as wound dressings, etc., allows ingrowth of cells.	
XX		
PS	Claim 5; Fig 1B; 39pp; English.	
XX		
CC	This represents the human elastin sequence containing the minimal	
CC	functional unit (MFU)-1 polypeptide of the invention. This MFU-1 is a	
CC	polypeptide that has at least 3 beta-sheet/ beta-turn structures, but is	
CC	not a naturally occurring fibrous protein. Each beta-sheet structure has	
CC	3-7 (preferably 5-7) amino acids and the MFU polypeptide may include at	
CC	least 1 amino acid that can take part in crosslinking. The polypeptide	
CC	can also be derived from the sequences of animal elastin, lampirin and	

CC spider silk protein. The MFU polypeptides are self-aligning peptides  
CC having the same primary structure as part of a natural fibrous protein.  
CC They are used to coat prostheses made of animal or synthetic material or  
CC metal, particularly for use as blood vessel or heart valve replacements,  
CC wound or burn dressings, or stents. They can be used in cosmetic, elastic  
CC or high-tensile strength materials, e.g. ropes or parachute cord.  
CC Prostheses based on the MFU allow penetration of endothelial cells, so  
CC become permanent, living, tissue replacements. The MFU polypeptides have  
CC better biocompatibility than known elastin-based materials. They are well  
CC defined, homogeneous material and are easier to manipulate and produce  
CC than full-length elastin. They are non-thrombogenic and non-immunogenic.  
CC Materials can be made from 2 or more different MFU polypeptides to allow  
CC properties to be tailored for particular applications, e.g. combining the  
CC high extensibility of elastin and the high tensile strength of spider  
CC silk protein

XX Sequence 730 AA;

Query Match 100.0%; Score 501; DB 2; Length 730;  
Best Local Similarity 100.0%; Pred. No. 4.4e-34;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAAAKSAKVAKAQQLRAAGIGAGIPGLGVGVPGIGVAGVPGIGAGVPGFGAG 60  
DB 498 VAAAKSAKVAKAQQLRAAGIGAGIPGLGVGVPGIGVAGVPGIGAGVPGFGAG 557

QY 61 ADEGVRRSLSPFLREGDPSSQHLPTSPSSPRVPALAAK 101  
DB 558 ADEGVRRSLSPFLREGDPSSQHLPTSPSSPRVPALAAK 598

RESULT 2  
AA69068  
ID AAY69068 standard; protein; 731 AA.

AC AAY69068;  
XX  
DT 30-MAY-2000 (first entry)

DE Amino acid sequence of a human tropoelastin splice form.

XX Tropoelastin; derivative; proteolysis; protease; antiwrinkle;  
XX hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;  
XX peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.  
XX Homo sapiens.

XX Key Location/Qualifiers  
FH Cleavage-site 441..442  
FT Cleavage-site 503..504  
FT Cleavage-site 515..516  
FT Cleavage-site 564..565

XX WO200004043-A1.

XX 27-JAN-2000.

XX 19-JUL-1999; 99WO-AU000580.

XX 17-JUL-1998; 98AU-00004723.

XX (UNSY ) UNIV SYDNEY.

XX Weiss AS;

XX WPI; 2000-182399/16.

XX N-PSDB; AA261146.

XX New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and

XX cell growth.

XX Disclosure; Page 107-109; 136pp; English.

CC The present sequence represents a human tropoelastin splice form. The  
CC specification describes tropoelastin derivatives, in which a subsequence  
CC has been mutated so that susceptibility to proteolysis is reduced or  
CC eliminated, or a subsequence has been inserted so that susceptibility to  
CC proteolysis is increased. The derivatives have with reduced  
CC susceptibility, and can be used where the wild-type protein would be  
CC degraded too easily, e.g. in contact with serum or wound exudate. The  
CC tropoelastin derivatives provide competitive inhibition of protease  
CC activity. The tropoelastin derivatives, and other polypeptides containing  
CC tropoelastin derivative-derived protease-susceptibility sites, are useful  
CC in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand  
CC lotions), as bulking agents and for inducing chemotaxis. They are also  
CC useful for proliferation or growth inhibition, particularly of smooth  
CC muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes,  
CC macrocytes and platelets. Peptidomimetics that mimic the protease  
CC cleavage site in tropoelastin derivatives are competitive inhibitors of  
CC the protease, and are used for protecting against lung damage caused by  
CC elastin, for inhibiting or controlling localized growth of cancers or  
CC metastases, or to limit protease activity that causes blood clotting

XX Sequence 731 AA;

Query Match 100.0%; Score 501; DB 3; Length 731;  
Best Local Similarity 100.0%; Pred. No. 4.4e-34;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAAAKSAKVAKAQQLRAAGIGAGIPGLGVGVPGIGVAGVPGIGAGVPGFGAG 60  
DB 498 VAAAKSAKVAKAQQLRAAGIGAGIPGLGVGVPGIGVAGVPGIGAGVPGFGAG 557

QY 61 ADEGVRRSLSPFLREGDPSSQHLPTSPSSPRVPALAAK 101  
DB 558 ADEGVRRSLSPFLREGDPSSQHLPTSPSSPRVPALAAK 598

RESULT 3  
AAB6657  
ID AAB6657 standard; protein; 731 AA.

XX AAB6657;

XX 05-APR-2001 (first entry)

XX Human elastin protein without signal peptide.

XX Minimal function unit; MFU; human; elastin prosthetic.

XX Homo sapiens.

XX WO200100666-A2.

XX 04-JAN-2001.

XX 29-JUN-2000; 2000WO-US017829.

XX 29-JUN-1999; 99US-00340736.

XX (PROT-) PROTEIN SPECIALTIES LTD.

XX (HSCR-) HSC RES & DEV LP.

XX Rothstein A, Keeley F, Rothstein S, Stahl R;

XX WPI; 2001-102886/11.

XX Novel polypeptides that comprise three beta-sheet/beta-turn structures

XX and are not naturally occurring fibrous protein, used to produce

XX prostheses suitable for implantation into humans, and cosmetic materials.

XX Claim 1; Fig 1; 39pp; English.

XX The present invention relates to a minimal functional unit (MFU) of human

XX elastin polypeptide. This protein is useful in a cosmetic material or a

XX prosthetic material such as prosthesis for blood vessel replacements, for

CC heart valve replacement, tissue replacement, for covering burns, for  
CC covering wounds and stents  
XX  
SQ Sequence 731 AA;  
Query Match 100.0%; Score 501; DB 4; Length 731;  
Best Local Similarity 100.0%; Pred. No. 4, 4e-34;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VAAAKSAKVAKAQOLRAAGIGAGIPGLGVGVPGIGVGVGAGVPGFGAG 60  
DB 498 VAAAKSAKVAKAQOLRAAGIGAGIPGLGVGVPGIGVGVGAGVPGFGAG 557  
QY 61 ADEGVRRSLSPELREDPSSOHLPTSPSPRPVPGALAAK 101  
DB 558 ADEGVRRSLSPELREDPSSOHLPTSPSPRPVPGALAAK 598  
RESULT 4  
ABU08725 100.0%; Score 501; DB 4; Length 731;  
Best Local Similarity 100.0%; Pred. No. 4, 4e-34;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
AC ABU08725; protein; 731 AA.  
XX  
XX  
DT 25-JUN-2003 (first entry)  
XX  
DE Human elastin mature protein.  
XX  
KM Human; elastin; minimal functioning unit; MFU;  
KM beta-sheet/beta-turn structure; fibrous protein; prosthesis;  
KM blood vessel replacement; heart replacement valve; burn; wound; lamprin;  
KM spider silk; cord; rope; parachute; cosmetic; platelet binding inhibitor;  
KM platelet activation inhibitor; non-chromogenic; cell infiltration;  
KM non-immunogenic; biocompatible; high tensile strength; elasticity;  
KM plasticity.  
XX  
XX Homo sapiens.  
XX  
XX US6489446-B1.  
XX  
PD 03-DEC-2002.  
XX  
PF 29-JUN-1999; 99US-00340736.  
XX  
XX 07-AUG-1996; 96US-0023522P.  
XX  
PR 07-AUG-1997; 97US-00911364.  
XX  
PA (HSCR-) HSC RES & DEV LP.  
XX (PROT-) PROTEIN SPECIALTIES LTD.  
XX  
XX Rothstein A, Keeley F, Rothstein S;  
XX  
XX PI  
XX  
XX DR WPI; 2003-391056/37.  
XX  
XX PT Novel polypeptide useful in prosthesis, has a secondary structure  
XX characterized by three beta-sheet/beta-turn structures, and is not a  
XX naturally occurring fibrous protein.  
XX  
XX PS Claim 1; Fig 1B; 21pp; English.  
XX  
XX CC The invention describes a polypeptide (I) comprising a minimal  
XX functioning unit (MFU) which is present in the sequence of human elastin  
XX and comprised of at least three beta-sheet/beta-turn structures, and at  
XX least one amino acid residue that participates in cross-linking, and not  
XX a naturally occurring fibrous protein. The MFU material can be used to  
XX construct human elastin-like prostheses such as tubes for blood vessel  
XX replacement, heart replacement valves and sheets for other uses such as  
XX burns or wounds to promote healing. MFUs can be co-aggregated with other  
XX proteins, for e.g. collagen, to provide prosthesis material that  
XX resembles the natural structural materials of the body. MFUs modeled on  
XX lamprin and other fibrous proteins e.g. spider silk, can be used to make  
XX a variety of materials, for a number of different applications, for e.g.  
XX in cords and ropes for use in parachutes and in cosmetics. Coating

CC synthetic prosthesis with MFUs modeled on human elastin significantly  
CC inhibits platelet binding and activation. The human-like MFU material is  
CC more biocompatible than other elastin-containing materials. In contrast  
CC to solubilised fragments of elastin used before, an MFU is a single  
CC peptide of defined composition. The MFU is considerably smaller than the  
CC parent protein, simpler in structure, easier to produce or express in  
CC quantity, to handle in solution and to manipulate for experimental and  
CC practical purposes. Like other elastin preparations, the MFU is non-  
CC thrombogenic and provides a friendly environment for cell infiltration.  
CC Being composed entirely of a human elastin sequence, MFU is non-  
CC immunogenic, thus providing a truly biocompatible material. MFUs modeled  
CC on lamprin and other fibrous proteins can be used to make a variety of  
CC materials having high tensile strength, elasticity and plasticity of  
CC their parent proteins. This is the amino acid sequence of mature human  
CC elastin on which the MFU peptides of the invention are based  
XX  
SQ Sequence 731 AA;  
Query Match 100.0%; Score 501; DB 6; Length 731;  
Best Local Similarity 100.0%; Pred. No. 4, 4e-34;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VAAAKSAKVAKAQOLRAAGIGAGIPGLGVGVPGIGVGVGAGVPGFGAG 60  
DB 498 VAAAKSAKVAKAQOLRAAGIGAGIPGLGVGVPGIGVGVGAGVPGFGAG 557  
QY 61 ADEGVRRSLSPELREDPSSOHLPTSPSPRPVPGALAAK 101  
DB 558 ADEGVRRSLSPELREDPSSOHLPTSPSPRPVPGALAAK 598  
RESULT 5  
ADL96420 100.0%; Score 501; DB 6; Length 731;  
Best Local Similarity 100.0%; Pred. No. 4, 4e-34;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
AC ADL96420; protein; 731 AA.  
XX  
XX  
XX ADL96420;  
XX  
XX DT 20-MAY-2004 (first entry)  
XX  
XX DE Human elastin protein fragment.  
XX  
XX KM fibrous protein; prosthesis; elastin; lamprin; spider silk protein;  
XX KM blood vessel; wound; burn healing; collagen.  
XX  
XX OS Homo sapiens.  
XX  
XX FH  
XX Key Location/Qualifiers  
XX FT Region 19..160  
XX FT /note="region specifically claimed in claim 6"  
XX FT Region 188..367  
XX FT /note="region specifically claimed in claim 6"  
XX FT Region 374..499  
XX FT /note="region specifically claimed in claim 6"  
XX FT Region 607..717  
XX FT /note="region specifically claimed in claim 6"  
XX  
XX PN US2003166846-A1.  
XX  
XX PD 04-SEP-2003.  
XX  
XX PF 28-SEP-2001; 2001US-00964662.  
XX  
XX PR 07-AUG-1996; 96US-0023522P.  
XX  
PR 07-AUG-1997; 97US-00911364.  
XX  
PR 29-JUN-1999; 99US-00340736.  
XX  
XX PA (ROTH/) ROTHSTEIN A.  
XX (KEELEY/) KEELEY F.  
XX (ROTH/) ROTHSTEIN S.  
XX  
XX PI Rothstein A, Keeley F, Rothstein S;  
XX  
XX DR WPI; 2003-898105/82.

XX polypeptide for constructing human elastin-like prostheses such as tubes  
PT for blood vessel replacement and sheets for other uses such as wound or  
PT burn healing, comprises three beta sheets and three beta turns.

XX Claim 5, Fig 1B; 17pp; English.

XX This invention describes a polypeptide that comprises three beta  
CC sheet/beta turn structures and that is not a naturally occurring fibrous  
CC protein. The invention also describes a prosthesis comprising an animal,  
CC metal or synthetic material, where the surface is coated with the  
CC polypeptide, a cosmetic material comprising the polypeptide, an elastic  
CC material comprising the polypeptide, a high tensile strength material  
CC comprising the polypeptide, a material comprising two or more  
CC polypeptides selected from (a) a polypeptide consisting essentially of a  
CC portion of the polypeptide comprising at least three beta sheet/beta turn  
CC structures, (b) a polypeptide consisting essentially of a portion of the  
CC amino acid sequence of an animal elastin comprising at least three beta  
CC sheets/beta turns, (c) a polypeptide consisting essentially of a portion  
CC of lamprin comprising at least three beta sheets/beta turns, and (d) a  
CC polypeptide consisting essentially of a spider silk protein comprising at  
CC least three beta sheets/beta turns; a polypeptide having the primary  
CC structure of a portion of a naturally occurring fibrous protein and a  
CC secondary structure comprising at least three beta sheets/beta turns,  
CC where each of the beta sheet/beta turn structures comprises from 3 to  
CC about 7 amino acids and the polypeptide is not a naturally occurring  
CC fibrous protein. The minimal functional unit (MFU) of the invention is  
CC useful to construct human elastin-like prostheses such as tubes for blood  
CC vessel replacement and sheets for other uses such as wound or burn  
CC healing. Alternatively the MFU can be co-aggregated with other proteins,  
CC for example collagen, to provide prosthesis material that resembles the  
CC natural structural materials of the body. The MFU based material is  
CC subject to infiltration of cells growing in the patient, including  
CC endothelial cells, and the prosthesis can become a permanent living  
CC tissue replacement. The material is more biocompatible than other elastin  
CC -containing materials proposed for prostheses.

XX Sequence 733 AA;

XX Query Match 100.0%; Score 501; DB 7; Length 733;

XX Best Local Similarity 100.0%; Pred. No. 4.4e-34;

XX Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 VAAAKSAKVAKAAQLRAAGAGAGIPGLGVGVPGAGVPGAGVPGFAG 60

DB 498 VAAAKSAKVAKAAQLRAAGAGAGIPGLGVGVPGAGVPGAGVPGFAG 557

QY 61 ADEGVRRLSPFLREGDPSSSQHLPTSPSSPRVPGALAAAK 101

DB 558 ADEGVRRLSPFLREGDPSSSQHLPTSPSSPRVPGALAAAK 598

RESULT 6

AAARS6653

AAARS6653 standard; protein; 733 AA.

AC AARS6653;

XX 25-MAR-2003 (revised)

DT 22-MAR-1995 (first entry)

XX Synthetic human tropoelastin (SHEL).

XX Tropoelastin; pharmaceutical; surgical dressing.

XX Synthetic.

PN WO9414958-A1.

XX 07-JUL-1994.

PD 16-DEC-1993; 93WO-AU000655.

PR 22-DEC-1992; 92AU-00006520.

PR 28-JUN-1993; 93AU-00009661.

XX (UNSY ) UNIV SYDNEY.

PI Weiss AS, Martin SL;

DR WPI; 1994-263633/32.

DR N-PSDB; AAQ70941.

XX Synthetic polynucleotide(s) - encode recombinant tropoelastins and

PT variants.

PS Disclosure; Page 30; 77pp; English.

XX Human synthetic tropoelastin is susceptible to hydrolytic breakdown of

CC the crosslinks. Such material may be useful in e.g. surgical

CC applications, where the gradual loss of material over time is intended.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 733 AA;

XX Query Match 100.0%; Score 501; DB 2; Length 733;

XX Best Local Similarity 100.0%; Pred. No. 4.4e-34;

XX Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 VAAAKSAKVAKAAQLRAAGAGAGIPGLGVGVPGAGVPGAGVPGFAG 60

DB 500 VAAAKSAKVAKAAQLRAAGAGAGIPGLGVGVPGAGVPGAGVPGFAG 559

QY 61 ADEGVRRLSPFLREGDPSSSQHLPTSPSSPRVPGALAAAK 101

DB 560 ADEGVRRLSPFLREGDPSSSQHLPTSPSSPRVPGALAAAK 600

RESULT 7

AAAY01301

AAAY01301 standard; protein; 733 AA.

AC AAY01301;

XX 07-JUN-1999 (first entry)

DT Amino acid sequence of synthetic human tropoelastin SHEL.

XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;

XX pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;

XX hand lotion; surgical implant; industrial product; human; SHEL.

XX Synthetic.

OS Homo sapiens.

PN WO903886-A1.

XX 28-JAN-1999.

PD 17-JUL-1998; 98WO-AU000564.

XX 18-JUL-1997; 97AU-00008117.

XX (UNSY ) UNIV SYDNEY.

PI Weiss AS;

XX WPI; 1999-132162/11.

DR N-PSDB; AAX27704.

XX New derivatives of human tropoelastin - with elastin-like or

PT macromolecular binding properties, useful e.g. as surgical implants.

PS Disclosure; Fig 1; 82pp; English.

XX The invention relates to a derivative or variant of human tropoelastin

(hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as anti-wrinkle or hand lotions, also as surgical implants, foods and industrial products. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated peptide 26a, from hTE. The present sequence represents the amino acid sequence of the synthetic human tropoelastin SHEL

SO Sequence 733 AA;

Query Match 100.0%; Score 501; DB 2; Length 733;  
Best Local Similarity 100.0%; Pred. No. 4.4e-34;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAAAASAAKVAKAKQLRAAGAGAGIPGIGVGVGPGIGVGAGVPGFGAG 60  
DB 500 VAAAASAAKVAKAKQLRAAGAGAGIPGIGVGVGPGIGVGAGVPGFGAG 559

QY 61 ADEGVRRLSPELREGDPSSSOHLPTPSSPRVPGALAAAK 101  
DB 560 ADEGVRRLSPELREGDPSSSOHLPTPSSPRVPGALAAAK 600

RESULT 8  
ABG75223  
ID ABG75223 standard; protein; 757 AA.  
XX  
AC ABG75223;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human tropoelastin protein.  
XX  
KW Human; tropoelastin; elastin; body vessel occlusion; stenosis;  
KW vascular smooth muscle cell; elastin signaling; vasotropic.  
XX  
OS Homo sapiens.  
XX  
PN WO2003082203-A2.  
XX  
PD 09-OCT-2003.  
XX  
PF 27-MAR-2003; 2003WO-US009391.  
XX  
PR 27-MAR-2002; 2002US-0368084P.  
XX  
PA (UTAH) UNIV UTAH RES FOUND.  
XX  
PI LA DY, Karnik S;  
XX  
DR WPI; 2003-833516/77.  
XX  
PT Use of an agent that promotes elastin signaling in smooth muscle cells for e.g. decreasing or preventing occlusion of a body vessel by smooth muscle cells, treating or preventing obstructive vascular disease, or preventing stenosis.  
XX  
PS Claim 24; Page 138-141; Opp; English.  
XX  
CC The present invention relates to the use of an agent that promotes elastin signaling in smooth muscle cells for decreasing or preventing occlusion of a body vessel by smooth muscle cells, decreasing vascular obstruction, increasing F:G obstruction, promoting actin stress fiber formation or actin polymerization, increasing F:G treatment or preventing obstructive vascular disease (e.g. stenosis), or preventing stenosis. The agent that promotes elastin signaling in smooth muscle cells is useful for decreasing or preventing occlusion of a body vessel by smooth muscle cells, decreasing vascular obstruction, promoting actin stress fiber formation or actin polymerization, increasing F:G

actin ratio in a smooth muscle cell, treating or preventing obstructive vascular disease (e.g. stenosis following angioplasty), or preventing stenosis. It is also useful in manufacturing a medicament for the treatment or prevention of occlusion of a vessel. The present sequence is the human tropoelastin protein as shown in the exemplification of the invention

SO Sequence 757 AA;

Query Match 100.0%; Score 501; DB 7; Length 757;  
Best Local Similarity 100.0%; Pred. No. 4.6e-34;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAAAASAAKVAKAKQLRAAGAGAGIPGIGVGVGPGIGVGAGVPGFGAG 60  
DB 524 VAAAASAAKVAKAKQLRAAGAGAGIPGIGVGVGPGIGVGAGVPGFGAG 583

QY 61 ADEGVRRLSPELREGDPSSSOHLPTPSSPRVPGALAAAK 101  
DB 584 ADEGVRRLSPELREGDPSSSOHLPTPSSPRVPGALAAAK 624

RESULT 9  
ADP65160  
ID ADP65160 standard; protein; 757 AA.  
XX  
AC ADP65160;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Human elastin.  
XX  
KW autoimmune disease; arthritis; gene expression analysis;  
KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;  
KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;  
KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;  
KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;  
KW immune; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003072827-A1.  
XX  
PD 04-SEP-2003.  
XX  
PF 31-OCT-2002; 2002WO-US035433.  
XX  
PR 31-OCT-2001; 2001US-0336220P.  
XX  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
XX  
PI Hirsch R, Thorton SL;  
XX  
DR WPI; 2003-712740/67.  
XX  
DR GENBANK; NP\_000492.  
XX  
PT Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and gout.  
XX  
PS Disclosure; Page; 56pp; English.  
XX  
CC The invention relates to a novel method for diagnosing and analysing autoimmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using that gene expression signature to diagnose or analyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention further comprises: a treatment of rheumatoid arthritis; identification of genes for targeting in the treatment of rheumatoid arthritis in a mammal other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an

CC array or gene chip, specific for rheumatoid arthritis; diagnosis or  
CC analyses of autoimmune disease or rheumatoid arthritis; screening the  
CC efficacy of a candidate drug in vitro for the treatment of collagen-  
CC induced arthritis; and reducing the symptoms associated with collagen-  
CC induced arthritis. The compositions of the invention have the following  
CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,  
CC antipain, antiinflammatory, dermatological, and immunomodulatory. The  
CC methods and compositions of the present invention are useful for  
CC diagnosing and treating autoimmune disease or arthritis, such as  
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,  
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an  
CC immune disease caused by an infectious agent. This sequence represents a  
CC protein sequence relating to the genes used in the analysis and treatment  
CC of autoimmune diseases or arthritis. Note: This sequence is not shown  
CC in the specification. It has been supplied in an electronic format from  
CC WIPO.

SQ Sequence 757 AA;  
Query Match 100.0%; Score 501; DB 7; Length 757;  
Best Local Similarity 100.0%; Pred. No. 4.6e-34;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAAAKSAKVAQAQLRRAAGIGAGIPGLGVGVPGLVGAGVPGFAG 60  
DB 524 VAAAKSAKVAQAQLRRAAGIGAGIPGLGVGVPGLVGAGVPGFAG 583  
QY 61 ADEGVRRSLSPRLREGDPSSQHLPTSPSPRPVPGALAAK 101  
DB 584 ADEGVRRSLSPRLREGDPSSQHLPTSPSPRPVPGALAAK 624

RESULT 10  
ID AAY01310 standard; protein; 216 AA.  
XX AAY01310;  
AC AAY01310;  
XX 07-JUN-1999 (first entry)  
DT 07-JUN-1999 (first entry)  
DE Human tropoelastin derivative SHEL26-36.  
XX  
XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;  
KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;  
KW hand lotion; surgical implant; industrial product; human; SHEL; variant.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
PN WO9903886-A1.  
XX  
PD 28-JAN-1999.  
XX  
PF 17-JUL-1998; 98WC-AU000564.  
XX  
PR 18-JUL-1997; 97AU-00008117.  
XX  
PA (UNSY ) UNITV SYDNEY.  
XX  
XX Weiss AS;  
PI  
XX  
DR WPI; 1999-132162/11.  
XX  
PT New derivatives of human tropoelastin - with elastin-like or  
XX macromolecular binding properties, useful e.g. as surgical implants.  
PS  
XX Claim 35; Page 11; 82pp; English.  
CC The invention relates to a derivative or variant of human tropoelastin  
CC (hTE) having elastin-like and/or macromolecule (specifically  
CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors  
CC comprising the nucleic acids encoding the variants or derivatives are  
CC used to produce the proteins recombinantly. The tropoelastin derivatives

CC or hybrid proteins containing the derivatives are useful in medical,  
CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
CC wrinkle or hand lotions, also as surgical implants, foods and industrial  
CC products. The hybrid protein have controllable GAG-binding properties,  
CC depending on presence or absence of a specific fragment, designated  
CC peptide 26a, from hTE. The present sequence represents a human  
CC tropoelastin derivative SHEL26-36

SQ Sequence 216 AA;  
Query Match 84.6%; Score 424; DB 2; Length 216;  
Best Local Similarity 100.0%; Pred. No. 4.2e-28;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 AAAGGAGIPGLGVGVPGLVGAGVPGFAGADGVRRSLSPRLREGDP 78  
DB 1 AAAGGAGIPGLGVGVPGLVGAGVPGFAGADGVRRSLSPRLREGDP 60  
QY 79 SSSQHLPTSPSPRPVPGALAAK 101  
DB 61 SSSQHLPTSPSPRPVPGALAAK 83

RESULT 11  
ID AAY01305 standard; protein; 200 AA.  
XX AAY01305;  
AC AAY01305;  
XX 07-JUN-1999 (first entry)  
DT 07-JUN-1999 (first entry)  
DE Human tropoelastin derivative SHELgamma.  
XX  
XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;  
KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;  
KW hand lotion; surgical implant; industrial product; human; SHEL; variant.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
PN WO9903886-A1.  
XX  
PD 28-JAN-1999.  
XX  
PF 17-JUL-1998; 98WC-AU000564.  
XX  
PR 18-JUL-1997; 97AU-00008117.  
XX  
PA (UNSY ) UNITV SYDNEY.  
XX  
XX Weiss AS;  
PI  
XX  
DR WPI; 1999-132162/11.  
XX  
PT N-PSDB; AAX27707.  
XX  
XX New derivatives of human tropoelastin - with elastin-like or  
XX macromolecular binding properties, useful e.g. as surgical implants.  
PS  
XX Claim 15; Fig 8; 82pp; English.  
CC The invention relates to a derivative or variant of human tropoelastin  
CC (hTE) having elastin-like and/or macromolecule (specifically  
CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors  
CC comprising the nucleic acids encoding the variants or derivatives are  
CC used to produce the proteins recombinantly. The tropoelastin derivatives  
CC or hybrid proteins containing the derivatives are useful in medical,  
CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
CC wrinkle or hand lotions, also as surgical implants, foods and industrial  
CC products. The hybrid protein have controllable GAG-binding properties,  
CC depending on presence or absence of a specific fragment, designated  
CC peptide 26a, from hTE. The present sequence represents a human  
XX tropoelastin derivative SHELgamma

SQ Sequence 200 AA;  
 Query Match 61.5%; Score 308; DB 2; Length 200;  
 Best Local Similarity 95.3%; Pred. No. 2,4e-18;  
 Matches 61; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 38 GLGVGAGVPGTGVGAGVPGFAGADGCVRRSLSPELREGDPSSSQHLPTPSSPRVPGAL 97  
 DB 4 GALVGVGAGVPGTGVGAGVPGFAGADGCVRRSLSPELREGDPSSSQHLPTPSSPRVPGAL 63  
 QY 98 AAAG 101  
 DB 64 AAAG 67  
 RESULT 12  
 ADB64761  
 ID ADB64761 standard; protein; 617 AA.  
 AC ADB64761;  
 XX  
 XX 04-DEC-2003 (first entry)  
 XX  
 DE Human protein encoded by clone NT2RP70003110.  
 XX  
 KM Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;  
 KW cell regeneration; membrane protein; signal transduction-related protein;  
 KM transcription-related protein; osteoporosis; neurological disease;  
 KM cancer; tumour.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EPI308459-A2.  
 XX  
 PD 07-MAY-2003.  
 XX  
 PF 28-MAR-2002; 2002EP-00007401.  
 XX  
 PR 05-NOV-2001; 2001JP-00379298.  
 PR 25-JUN-2002; 2002US-00350978.  
 XX  
 PA (HELI-) HELIX RES INST.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 XX  
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,  
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I,  
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y;  
 XX  
 DR WPI; 2003-450961/43.  
 DR N-PSDB; ADB62791.  
 XX  
 PT New polynucleotides and polypeptides, useful for developing a diagnostic  
 PT marker or medicines for regulation of their expression and activity, or  
 PT as targets of gene therapy.  
 XX  
 XX Claim 1; Page; 222pp; English.  
 XX  
 CC The invention discloses a polynucleotide comprising a sequence selected  
 CC from 1970 fully defined nucleotide sequences which encode novel  
 CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide  
 CC or its partial peptide, an antibody binding to the polypeptide or peptide  
 CC of the polynucleotide, immunologically assaying the polypeptide or peptide  
 CC with the antibody of the polynucleotide by contacting the polypeptide or peptide  
 CC between the two, a transformant carrying the polynucleotide in an  
 CC expressible manner and an antisense polynucleotide. The oligonucleotide  
 CC is useful as a primer for synthesizing the polynucleotide, or as a probe  
 CC for detecting the polynucleotide. The polynucleotides and encoded  
 CC proteins are useful as pharmaceutical agents and many disease-related  
 CC genes may be included in them, for developing a diagnostic marker or  
 CC medicines for regulation of their expression and activity, or as targets  
 CC of gene therapy. The genes are involved in tissue and/or cell  
 CC regeneration. Membrane proteins, signal transduction-related proteins,

CC transcription-related proteins, disease-related proteins and genes  
 CC encoding them can be used as indicators for diseases (e.g. osteoporosis,  
 CC neurological diseases, cancer, tumours. The cDNA may be used to regulate  
 CC the activity or expression of the encoded protein to treat diseases. The  
 CC sequence presented is a protein of the invention. Note: Some of the  
 CC sequence data for this patent is not represented in the printed  
 CC specification, but is based on sequence information supplied by the  
 CC European Patent Office.  
 XX  
 SQ Sequence 617 AA;  
 Query Match 60.8%; Score 304.5; DB 7; Length 617;  
 Best Local Similarity 67.3%; Pred. No. 1.4e-17;  
 Matches 68; Conservative 0; Mismatches 0; Indels 33; Gaps 1;  
 QY 1 VAAAKSAKVAKAAKAAKAAAGAGAGTGGVGVGVPGTGVGAGVPGFAG 60  
 DB 435 VAAAKSAKVAKAAKAAKAAAGAGAGTGGVGVGVPGTGVGAGVPGFAG- 493  
 QY 61 ADEGVRRSLSPELREGDPSSSQHLPTPSSPRVPGALAAAK 101  
 DB 494 -----VPGALAAAK 502  
 RESULT 13  
 AAAY01303  
 ID AAAY01303 standard; protein; 660 AA.  
 XX  
 AC AAAY01303;  
 XX  
 XX 07-JUN-1999 (first entry)  
 XX  
 DE Human tropoelastin derivative SHEldeltamodified.  
 XX  
 KM Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;  
 KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;  
 KM hand lotion; surgical implant; industrial product; human; SHEL.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 OS  
 PN WO9903886-A1.  
 XX  
 PD 28-JAN-1999.  
 XX  
 PF 17-JUL-1998; 98WO-AU000564.  
 XX  
 PR 18-JUL-1997; 97AU-00008117.  
 XX  
 PA (UNSY ) UNIV SYDNEY.  
 XX  
 PI Weiss AG;  
 PI  
 DR WPI; 1999-132162/11.  
 DR N-PSDB; AAX27705.  
 XX  
 PT New derivatives of human tropoelastin - with elastin-like or  
 PT macromolecular binding properties, useful e.g. as surgical implants.  
 XX  
 XX Claim 7; Fig 3; 82pp; English.  
 XX  
 CC The invention relates to a derivative or variant of human tropoelastin  
 CC (hTE) having elastin-like and/or macromolecule (specifically  
 CC glycosaminoglycan (GAG)-binding properties. Cells containing vectors  
 CC comprising the nucleic acids encoding the variants or derivatives are  
 CC used to produce the proteins recombinantly. The tropoelastin derivatives  
 CC or hybrid proteins containing the derivatives are useful in medical,  
 CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
 CC wrinkle or hand lotions, also as surgical implants, foods and industrial  
 CC products. The hybrid protein have controllable GAG-binding properties,  
 CC depending on presence or absence of a specific fragment, designated  
 CC peptide 26A, from hTE. The present sequence represents a human  
 CC tropoelastin derivative SHEldeltamodified

XX SQ Sequence 660 AA;  
Query Match 60.8%; Score 304.5; DB 2; Length 660;  
Best Local Similarity 67.3%; Pred. No. 1.5e-17;  
Matches 68; Conservative 0; Mismatches 0; Indels 33; Gaps 1;  
QY 1 VAAAKSAKVAKQGLRAAGLGGAGIPGLGVGVGVPGLGVAGVPGFAG 60  
DB 461 VAAAKSAKVAKQGLRAAGLGGAGIPGLGVGVGVPGLGVAGVPGFAG- 519  
QY 61 ADEGVRRSLSPBLREGDPSSQHLPTSPSSPRVPGALAAK 101  
DB 520 -----VPGALAAK 528  
RESULT 14  
ADM03792  
ID ADM03792 standard; protein; 663 AA.  
XX  
AC ADM03792;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human protein of the invention SEQ ID NO:2477.  
XX  
KW human; gene therapy; diagnostic marker; pharmaceutical.  
XX  
OS Homo sapiens.  
XX  
PN EP1347046-A1.  
XX  
PD 24-SEP-2003.  
XX  
PF 12-APR-2002; 2002EP-00008400.  
XX  
PR 22-MAR-2002; 2002JP-00137785.  
XX  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX  
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,  
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I,  
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y;  
XX  
DR WPI; 2003-723558/69.  
DR N-PSDB; ADM01349.  
XX  
PT New polynucleotides and polypeptides are useful in gene therapy, for  
PT developing a diagnostic marker or medicines for regulating their  
PT expression and activity, or as a target of gene therapy.  
XX  
PS Claim 1; SEQ ID NO 2477; 305pp; English.  
XX  
CC The invention relates to a novel human polynucleotide and the encoded  
CC polypeptide. A polynucleotide of the invention may have a use in gene  
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful  
CC as a primer for synthesizing the polynucleotide or as a probe for  
CC detecting the polynucleotide. The polynucleotides ADM0316-ADM03758 are  
CC useful in gene therapy, for developing a diagnostic marker or medicines  
CC for regulating their expression and activity, or as a target of gene  
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides  
CC are useful as pharmaceutical agents. The present sequence represents a  
CC protein sequence of the invention.  
XX  
SQ Sequence 663 AA;  
Query Match 60.8%; Score 304.5; DB 7; Length 663;  
Best Local Similarity 67.3%; Pred. No. 1.5e-17;  
Matches 68; Conservative 0; Mismatches 0; Indels 33; Gaps 1;  
QY 1 VAAAKSAKVAKQGLRAAGLGGAGIPGLGVGVGVPGLGVAGVPGFAG 60  
DB 463 VAAAKSAKVAKQGLRAAGLGGAGIPGLGVGVGVPGLGVAGVPGFAG- 521

QY 61 ADEGVRRSLSPBLREGDPSSQHLPTSPSSPRVPGALAAK 101  
DB 522 -----VPGALAAK 530  
RESULT 15  
ADE40134  
ID ADE40134 standard; protein; 692 AA.  
XX  
AC ADE40134;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human NOV16b protein - SEQ ID 40.  
XX  
KW NOV; cardiac; antiarteriosclerotic; hypotensive; cyrostatic; anorectic;  
KW antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nocrotic;  
KW antiparkinsonian; antiaesthetic; gynaecological; cardiomyopathy;  
KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;  
KW multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;  
KW asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;  
KW tissue typing; human; NOV.  
XX  
OS Homo sapiens.  
XX  
PN WO2003064589-A2.  
XX  
PD 07-AUG-2003.  
XX  
PF 02-AUG-2002; 2002WO-US024483.  
XX  
PR 02-AUG-2001; 2001US-0309501P.  
PR 03-AUG-2001; 2001US-0310291P.  
PR 07-AUG-2001; 2001US-0310544P.  
PR 08-AUG-2001; 2001US-0310951P.  
PR 09-AUG-2001; 2001US-0311292P.  
PR 13-AUG-2001; 2001US-0311979P.  
PR 16-AUG-2001; 2001US-0312892P.  
PR 17-AUG-2001; 2001US-0313201P.  
PR 17-AUG-2001; 2001US-0313415P.  
PR 20-AUG-2001; 2001US-0313643P.  
PR 20-AUG-2001; 2001US-0313702P.  
PR 21-AUG-2001; 2001US-0314031P.  
PR 23-AUG-2001; 2001US-0314466P.  
PR 28-AUG-2001; 2001US-0315403P.  
PR 29-AUG-2001; 2001US-0315853P.  
PR 17-SEP-2001; 2001US-0322716P.  
PR 21-SEP-2001; 2001US-0323994P.  
PR 14-DEC-2001; 2001US-0340233P.  
PR 05-FEB-2002; 2002US-0354591P.  
PR 19-MAR-2002; 2002US-0365478P.  
PR 19-APR-2002; 2002US-0373814P.  
PR 19-APR-2002; 2002US-0373825P.  
PR 19-APR-2002; 2002US-0373899P.  
PR 23-APR-2002; 2002US-0374632P.  
PR 07-JUN-2002; 2002US-0386971P.  
PR 01-AUG-2002; 2002US-00210172.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
PA  
XX  
PI Kishida R, Miller CE, Patnuttarajan M, Pena CRA, Rieger DK;  
PI Shimizu RA, Zernusen BD, Li L, Ji W, Padiganu M, Casman SJ;  
PI Voss EZ, Boldog FL, Gorman L, Leite MW, Vernet CM, Anderson DW,  
PI Guo X, Zhong M, Gerlach VL, Hjalte T, Rastelli L, Spytek KA;  
PI Dinger SR, Ellerman K, Malyankar DM, MacDougall JR, Stone DJ;  
PI Alsbrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AK;  
PI Smithson G;  
XX  
DR WPI; 2003-663472/62.  
DR N-PSDB; ADE40133.  
XX  
PT New NOVX polypeptides and nucleic acids, useful for preventing or



PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or  
PT pharmacogenomics.

PS Claim 1; SEQ ID NO 40; 560pp; English.

XX  
XX  
CC The invention relates to a novel NOVX polypeptide. The polypeptide of the  
CC invention demonstrates cardiant, antiarteriosclerotic, hypotensive,  
CC cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,  
CC neuroprotective, nootropic, antiparkinsonian, antiasthmatic and  
CC gynaecological activities and may be useful in diagnosing, treating or  
CC preventing NOVX-associated disorders including cardiomyopathy,  
CC atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple  
CC sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's  
CC disease, asthma or fertility disorders. Furthermore, the polypeptides may  
CC be utilised as vaccines whilst the nucleic acids may be used as  
CC hybridisation probes, in gene therapy, chromosome mapping, tissue typing,  
CC preventive medicine and pharmacogenomics. The current sequence is that of  
CC the human NOV protein of the invention.

XX  
SQ Sequence 692 AA;

Query Match 60.8%; Score 304.5; DB 7; Length 692;

Best Local Similarity 67.3%; Pred. No. 1.6e-17;

Matches 68; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 1 VAAAKSAKVAQAQIRAAAGLGGAGIPGLGVGVGPGLVGAAGVPGAG 60

DB 492 VAAAKSAKVAQAQIRAAAGLGGAGIPGLGVGVGPGLVGAAGVPGAG 550

QY 61 ADEGVRRSLSPELREGDPSSQHLPTPSSPRVPGALAAK 101

DB 551 -----VPGALAAK 559

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Job time : 120.095 secs

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## OM protein - protein search, using SW model

Run on: August 10, 2005, 07:27:07 ; Search time 30.1493 Seconds

(without alignments)  
250.074 Million cell updates/sec

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Perfect score: 501  
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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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- 2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501	100.0	731	2 US-08-911-364-1	Sequence 1, Appl
2	501	100.0	731	4 US-09-340-736E-1	Sequence 1, Appl
3	501	100.0	731	4 US-09-964-662-1	Sequence 1, Appl
4	501	100.0	733	3 US-08-464-700-2	Sequence 2, Appl
5	501	100.0	792	2 US-08-678-039A-40	Sequence 40, Appl
6	304.5	60.8	730	4 US-09-961-403-8	Sequence 8, Appl
7	159	31.7	281	1 US-08-397-633A-75	Sequence 75, Appl
8	158	31.5	287	1 US-08-397-633A-76	Sequence 76, Appl
9	155	30.9	877	1 US-08-397-633A-54	Sequence 54, Appl
10	154	30.7	884	1 US-08-397-633A-68	Sequence 68, Appl
11	154	30.7	884	2 US-08-435-641-15	Sequence 15, Appl
12	154	30.7	884	2 US-08-707-237A-96	Sequence 96, Appl
13	154	30.7	884	3 US-08-642-246-15	Sequence 15, Appl
14	154	30.7	884	4 US-09-451-206-15	Sequence 15, Appl
15	154	30.7	884	5 PCT-US96-06229-15	Sequence 15, Appl
16	153	30.5	768	3 US-08-806-029-35	Sequence 35, Appl
17	153	30.5	889	3 US-08-806-029-19	Sequence 19, Appl
18	153	30.5	1011	1 US-08-477-509B-94	Sequence 94, Appl
19	153	30.5	1011	3 US-08-482-085B-94	Sequence 94, Appl
20	153	30.5	1011	3 US-09-444-791A-94	Sequence 94, Appl
21	153	30.5	1170	1 US-08-175-155-59	Sequence 59, Appl
22	153	30.5	1170	2 US-08-707-237A-66	Sequence 66, Appl
23	153	30.5	2055	1 US-08-175-155-46	Sequence 46, Appl
24	153	30.5	2055	1 US-08-477-509B-81	Sequence 81, Appl
25	153	30.5	2055	2 US-08-707-237A-52	Sequence 52, Appl
26	153	30.5	2055	3 US-08-482-085B-81	Sequence 81, Appl
27	153	30.5	2055	3 US-09-444-791A-81	Sequence 81, Appl

28	153	30.5	2257	1 US-08-175-155-47	Sequence 47, Appl
29	153	30.5	2257	1 US-08-477-509B-82	Sequence 82, Appl
30	153	30.5	2257	2 US-08-707-237A-53	Sequence 53, Appl
31	153	30.5	2257	3 US-08-482-085B-82	Sequence 82, Appl
32	153	30.5	2257	3 US-09-444-791A-82	Sequence 82, Appl
33	151	30.1	479	1 US-08-397-633A-73	Sequence 73, Appl
34	151	30.1	479	1 US-08-397-633A-78	Sequence 78, Appl
35	151	30.1	750	3 US-08-806-029-25	Sequence 25, Appl
36	150	29.9	378	2 US-08-707-237A-104	Sequence 104, Appl
37	150	29.9	378	3 US-08-642-246-26	Sequence 26, Appl
38	150	29.9	378	4 US-09-451-206-26	Sequence 26, Appl
39	150	29.9	378	5 PCT-US96-06229-26	Sequence 26, Appl
40	150	29.9	486	1 US-08-397-633A-77	Sequence 77, Appl
41	150	29.9	696	3 US-08-806-029-36	Sequence 36, Appl
42	150	29.9	1002	2 US-08-707-237A-103	Sequence 103, Appl
43	150	29.9	1002	3 US-08-642-246-25	Sequence 25, Appl
44	150	29.9	1002	4 US-09-451-206-25	Sequence 25, Appl
45	150	29.9	1002	5 PCT-US96-06229-25	Sequence 25, Appl

## ALIGNMENTS

RESULT 1  
US-08-911-364-1  
Sequence 1, Application US/08911364  
Patent No. 5969106  
GENERAL INFORMATION:  
APPLICANT: ROTHSTEIN, Aseer  
APPLICANT: KEELY, Fred W.  
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELLED ON HUMAN  
TITLE OF INVENTION: ELASTIN AND OTHER FIBROUS PROTEINS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,364  
FILING DATE: 07-AUG-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,552  
FILING DATE: 07-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bent, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 041082/0104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 731 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-911-364-1  
Query Match 100.0%; Score 501; DB 2; Length 731;  
Best Local Similarity 100.0%; Pred. No. 2, 2e-41;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAAAKSAKVAAKQOLRAAGLGGAGIPGLGVGVGPGIGVGAGVPGFGAG 60  
DB 498 VAAAKSAKVAAKQOLRAAGLGGAGIPGLGVGVGPGIGVGAGVPGFGAG 557  
QY 61 ADEGVRRLSPELREGDPSSQHLPTSPSPRPVPGALAAK 101  
DB 558 ADEGVRRLSPELREGDPSSQHLPTSPSPRPVPGALAAK 598

## RESULT 2

US-09-340-736E-1  
; Sequence 1, Application US/09340736E  
; Patent No. 6489446  
; GENERAL INFORMATION:  
; APPLICANT: ROTHSTEIN, ASER  
; APPLICANT: KEELEY, FRED  
; APPLICANT: ROTHSTEIN, STEVEN  
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN  
; FILE REFERENCE: 041082/0110  
; CURRENT APPLICATION NUMBER: US/09/340,736E  
; CURRENT FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: 08/911,364  
; PRIOR FILING DATE: 1997-08-07  
; PRIOR APPLICATION NUMBER: 60/023,552  
; PRIOR FILING DATE: 1996-08-07  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 731  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-340-736E-1

Query Match 100.0%; Score 501; DB 4; Length 731;  
Best Local Similarity 100.0%; Pred. No. 2.2e-41;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAAAKSAKVAAKQOLRAAGLGGAGIPGLGVGVGPGIGVGAGVPGFGAG 60  
DB 498 VAAAKSAKVAAKQOLRAAGLGGAGIPGLGVGVGPGIGVGAGVPGFGAG 557  
QY 61 ADEGVRRLSPELREGDPSSQHLPTSPSPRPVPGALAAK 101  
DB 558 ADEGVRRLSPELREGDPSSQHLPTSPSPRPVPGALAAK 598

## RESULT 3

US-09-964-662-1  
; Sequence 1, Application US/09964662  
; Patent No. 6765086  
; GENERAL INFORMATION:  
; APPLICANT: PROTEIN SPECIALTIES LTD.  
; APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP  
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND  
; FILE REFERENCE: 041082/0112  
; CURRENT APPLICATION NUMBER: US/09/964,662  
; CURRENT FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: 09/340,736  
; PRIOR FILING DATE: 1999-06-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 731  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-964-662-1

Query Match 100.0%; Score 501; DB 4; Length 731;  
Best Local Similarity 100.0%; Pred. No. 2.2e-41;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAAAKSAKVAAKQOLRAAGLGGAGIPGLGVGVGPGIGVGAGVPGFGAG 60  
DB 498 VAAAKSAKVAAKQOLRAAGLGGAGIPGLGVGVGPGIGVGAGVPGFGAG 557  
QY 61 ADEGVRRLSPELREGDPSSQHLPTSPSPRPVPGALAAK 101  
DB 558 ADEGVRRLSPELREGDPSSQHLPTSPSPRPVPGALAAK 598

## RESULT 4

US-08-464-700-2  
; Sequence 2, Application US/08464700  
; Patent No. 6232458  
; GENERAL INFORMATION:  
; APPLICANT: WEISS, ANTHONY S  
; APPLICANT: MARTIN, STEPHEN L  
; TITLE OF INVENTION: SYNTHETIC POLYNUCLEOTIDES  
; NUMBER OF SEQUENCES: 54  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howson and Howson  
; STREET: Spring House Corporate Cntr, PO Box 457  
; CITY: Spring House  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19477  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464,700  
; FILING DATE: 7-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU PL6520  
; FILING DATE: 22-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU PL9661  
; FILING DATE: 28-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/AU93/00655  
; FILING DATE: 16-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bak, Mary E.  
; REGISTRATION NUMBER: 31,215  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-540-9200  
; TELEFAX: 215-540-5818  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 733 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-464-700-2

Query Match 100.0%; Score 501; DB 3; Length 733;  
Best Local Similarity 100.0%; Pred. No. 2.3e-41;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAAAKSAKVAAKQOLRAAGLGGAGIPGLGVGVGPGIGVGAGVPGFGAG 60  
DB 500 VAAAKSAKVAAKQOLRAAGLGGAGIPGLGVGVGPGIGVGAGVPGFGAG 559  
QY 61 ADEGVRRLSPELREGDPSSQHLPTSPSPRPVPGALAAK 101  
DB 560 ADEGVRRLSPELREGDPSSQHLPTSPSPRPVPGALAAK 600

RESULT 5  
US-08-678-039A-40

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; Sequence 40, Application US/08678039A
; Patent No. 5858662
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; TITLE OF INVENTION: Diagnosis of Williams Syndrome and
; TITLE OF INVENTION: Williams Syndrome Cognitive Profile by Analysis of the
; TITLE OF INVENTION: Presence or Absence of a LIM-Kinase Gene
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,039A
; FILING DATE: 10-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2323-120A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-624-1589
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 792 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-678-039A-40

Query Match      100.0%; Score 501; DB 2; Length 792;
Best Local Similarity 100.0%; Pred. No. 2.4e-41;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAAAKSAKVAKAQOLRAAAGLGGAGIPGLGVGVPGGLGVGAGVPGIGVAGVPGFGAG 60
DB 559 VAAAKSAKVAKAQOLRAAAGLGGAGIPGLGVGVPGGLGVGAGVPGIGVAGVPGFGAG 618

QY 61 ADEGVRSLSPLELREGDPSSSQHLPTSPSSPRVPGALAAAK 101
DB 619 ADEGVRSLSPLELREGDPSSSQHLPTSPSSPRVPGALAAAK 659

RESULT 6
US-09-961-403-8
; Sequence 8, Application US/09961403
; Patent No. 6780594
; GENERAL INFORMATION:
; APPLICANT: HE-STUMP, HOGER
; APPLICANT: HAENDLER, BERNARD
; APPLICANT: KRAETZSCHMAR, JOERN
; APPLICANT: KREFT, BERTHOLT
; APPLICANT: WINTERHAGER, ELKE
; APPLICANT: REGIDOR, PEDRO
; APPLICANT: SCOTTY, SIMON
; TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
; FILE REFERENCE: SCH-1789
; CURRENT APPLICATION NUMBER: US/09/961,403
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 8
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; LENGTH: 730
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-961-403-8

Query Match      60.8%; Score 304.5; DB 4; Length 730;
Best Local Similarity 67.3%; Pred. No. 4.8e-22;
Matches 68; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 1 VAAAKSAKVAKAQOLRAAAGLGGAGIPGLGVGVPGGLGVGAGVPGIGVAGVPGFGAG 60
DB 530 VAAAKSAKVAKAQOLRAAAGLGGAGIPGLGVGVPGGLGVGAGVPGIGVAGVPGFGAG 588

QY 61 ADEGVRSLSPLELREGDPSSSQHLPTSPSSPRVPGALAAAK 101
DB 589 -----VPGALAAAK 597

RESULT 7
US-08-397-633A-75
; Sequence 75, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-397-633A-75

Query Match      31.7%; Score 159; DB 1; Length 281;
Best Local Similarity 41.7%; Pred. No. 3.5e-08;
Matches 43; Conservative 8; Mismatches 40; Indels 12; Gaps 4;

QY 3 AAASAKVAKAQOLRAAAGLGGAGIPGLGV-----GVGPGGLGV-GAGVPGGLGV-GAGV 54
DB 164 AGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAG 223

QY 55 PGFGAGADEGVRSLSPLELREGDPSSSQHLPTSPSSPRVPGAL 97
DB 224 PGAGAGSGAGAGSGAGAM----DPGRYHMAAKGRAPGTGGT 262
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TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-397-633A-68

Query Match 30.7%; Score 154; DB 1; Length 884;  
Best Local Similarity 45.7%; Pred. No. 3.7e-07;  
Matches 42; Conservative 7; Mismatches 31; Indels 12; Gaps 4;

QY 3 AAASAKVAAKQLRAAGLIGAGIPGLGV-GVGVPGGLGV-----GAGVPGGLGV-GAGV 54  
DB 791 AGSAGAGSGAGAGSGAGSGAGSGVGVPGVGVPGKGVPGVGVPGVGVPGVGV 850

QY 55 PGFGAGADEGVRRSLSPELREGDPSSSOHLPS 86  
DB 851 PGAGAGSGAGAGSGAGAGAM---DPGRYODLRS 878

## RESULT 11

US-08-435-641-15  
Sequence 15, Application US/08435641  
Patent No. 5817303  
GENERAL INFORMATION:  
APPLICANT: Stedronsky, Edwin R.  
TITLE OF INVENTION: Tissue Adhesive Using Synthetic  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,641  
FILING DATE: 05-MAY-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Rowland, Bertram I.  
REGISTRATION NUMBER: 20015  
REFERENCE/DOCKET NUMBER: A-61127  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 884 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-435-641-15

Query Match 30.7%; Score 154; DB 2; Length 884;  
Best Local Similarity 45.7%; Pred. No. 3.7e-07;  
Matches 42; Conservative 7; Mismatches 31; Indels 12; Gaps 4;

QY 3 AAASAKVAAKQLRAAGLIGAGIPGLGV-GVGVPGGLGV-----GAGVPGGLGV-GAGV 54  
DB 791 AGSAGAGSGAGAGSGAGSGAGSGVGVPGVGVPGKGVPGVGVPGVGVPGVGV 850

QY 55 PGFGAGADEGVRRSLSPELREGDPSSSOHLPS 86  
DB 851 PGAGAGSGAGAGSGAGAGAM---DPGRYODLRS 878

## RESULT 12

US-08-707-237A-96  
Sequence 96, Application US/08707237A  
Patent No. 5830713  
GENERAL INFORMATION:  
APPLICANT: Ferrari, Franco A.  
APPLICANT: Capello, Joseph  
APPLICANT: Crisman, John W.  
APPLICANT: Dorman, Mary A.  
TITLE OF INVENTION: METHODS FOR PREPARING SYNTHETIC  
NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/707,237A  
FILING DATE: 03-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,155  
FILING DATE: 29-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/609,716  
FILING DATE: 06-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/269,429  
FILING DATE: 09-NOV-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Treccartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-10/MHD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 96:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 884 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-707-237A-96

Query Match 30.7%; Score 154; DB 2; Length 884;  
Best Local Similarity 45.7%; Pred. No. 3.7e-07;  
Matches 42; Conservative 7; Mismatches 31; Indels 12; Gaps 4;

QY 3 AAASAKVAAKQLRAAGLIGAGIPGLGV-GVGVPGGLGV-----GAGVPGGLGV-GAGV 54  
DB 791 AGSAGAGSGAGAGSGAGSGAGSGVGVPGVGVPGKGVPGVGVPGVGVPGVGV 850

QY 55 PGFGAGADEGVRRSLSPELREGDPSSSOHLPS 86







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## OM protein - protein search, using sw model

Run on: August 10, 2005, 07:37:53 ; Search time 105.522 Seconds  
(without alignments)  
373.667 Million cell updates/sec

Title: US-09-743-818a-4\_COPY\_500\_600

Perfect score: 501  
Sequence: 1 VAAAKSAKVAKAQLRRA.....QHLPSPSPRVGALAAAK 101

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1752860 seqs, 390397842 residues

Total number of hits satisfying chosen parameters: 1752860

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database:

Published Applications AA:\*  
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2: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/prodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/prodata/1/pubpaa/PCTUS\_NEW\_PUB.pep:\*  
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11: /cgn2\_6/prodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
13: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
14: /cgn2\_6/prodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
15: /cgn2\_6/prodata/1/pubpaa/US10D\_PUBCOMB.pep:\*  
16: /cgn2\_6/prodata/1/pubpaa/US10E\_PUBCOMB.pep:\*  
17: /cgn2\_6/prodata/1/pubpaa/US10F\_PUBCOMB.pep:\*  
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19: /cgn2\_6/prodata/1/pubpaa/US11A\_PUBCOMB.pep:\*  
20: /cgn2\_6/prodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
21: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
22: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501	100.0	731	US-09-964-662-1	Sequence 1, Appl1
2	490	97.8	788	US-10-852-065-4	Sequence 2, Appl1
3	490	97.8	788	US-10-852-575-3	Sequence 3, Appl1
4	304.5	60.8	617	US-10-104-047-2915	Sequence 2915, Ap
5	304.5	60.8	663	US-10-108-260A-2477	Sequence 2477, Ap
6	304.5	60.8	692	US-10-210-172-40	Sequence 40, Appl1
7	304.5	60.8	730	US-09-961-403-8	Sequence 8, Appl1
8	304.5	60.8	730	US-10-723-860-2566	Sequence 2566, Ap
9	301.5	60.2	711	US-10-210-172-38	Sequence 38, Appl1
10	154	30.7	244	US-10-800-179-27	Sequence 27, Appl1
11	154	30.7	244	US-10-845-775A-27	Sequence 27, Appl1

12	154	30.7	244	16	US-10-845-936A-27	Sequence 27, Appl1
13	154	30.7	244	18	US-10-939-036-27	Sequence 27, Appl1
14	154	30.7	246	16	US-10-800-179-26	Sequence 26, Appl1
15	154	30.7	246	16	US-10-800-179-28	Sequence 28, Appl1
16	154	30.7	246	16	US-10-845-775A-26	Sequence 26, Appl1
17	154	30.7	246	16	US-10-845-775A-28	Sequence 28, Appl1
18	154	30.7	246	16	US-10-845-936A-26	Sequence 26, Appl1
19	154	30.7	246	16	US-10-845-936A-28	Sequence 28, Appl1
20	154	30.7	246	18	US-10-939-036-26	Sequence 26, Appl1
21	154	30.7	246	18	US-10-939-036-28	Sequence 28, Appl1
22	154	30.7	884	14	US-10-117-931-15	Sequence 15, Appl1
23	154	30.7	983	16	US-10-845-936A-37	Sequence 37, Appl1
24	154	30.7	1027	16	US-10-845-936A-32	Sequence 32, Appl1
25	154	30.7	1105	16	US-10-845-936A-33	Sequence 33, Appl1
26	154	30.7	1125	16	US-10-845-936A-34	Sequence 34, Appl1
27	153	30.5	768	8	US-08-806-029-35	Sequence 35, Appl1
28	153	30.5	884	16	US-10-800-179-25	Sequence 25, Appl1
29	153	30.5	884	16	US-10-845-775A-25	Sequence 25, Appl1
30	153	30.5	884	16	US-10-845-936A-25	Sequence 25, Appl1
31	153	30.5	884	18	US-10-939-036-25	Sequence 25, Appl1
32	153	30.5	889	8	US-08-806-029-19	Sequence 19, Appl1
33	153	30.5	965	16	US-10-800-179-31	Sequence 31, Appl1
34	153	30.5	965	16	US-10-845-775A-31	Sequence 31, Appl1
35	153	30.5	965	16	US-10-845-936A-31	Sequence 31, Appl1
36	153	30.5	965	18	US-10-939-036-31	Sequence 31, Appl1
37	153	30.5	1011	14	US-10-096-986-94	Sequence 94, Appl1
38	153	30.5	1038	16	US-10-800-179-30	Sequence 30, Appl1
39	153	30.5	1038	16	US-10-845-775A-30	Sequence 30, Appl1
40	153	30.5	1038	16	US-10-845-936A-30	Sequence 30, Appl1
41	153	30.5	1038	18	US-10-939-036-30	Sequence 30, Appl1
42	153	30.5	2055	14	US-10-096-986-81	Sequence 81, Appl1
43	153	30.5	2257	14	US-10-096-986-82	Sequence 82, Appl1
44	151	30.1	750	8	US-08-806-029-25	Sequence 25, Appl1
45	150	29.9	378	14	US-10-117-931-26	Sequence 26, Appl1

## ALIGNMENTS

RESULT 1  
US-09-964-662-1  
; Sequence 1, Application US/09964662  
; Publication No. US2003016846A1  
; GENERAL INFORMATION:  
; APPLICANT: PROTEIN SPECIALTIES LTD.  
; APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP  
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELLED ON HUMAN ELASTIN AND  
; TITLE OF INVENTION: OTHER FIBROUS PROTEINS  
; FILE REFERENCE: 041082/0112  
; CURRENT APPLICATION NUMBER: US/09/964, 662  
; CURRENT FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: 09/340, 736  
; PRIOR FILING DATE: 1999-06-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 731  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-964-662-1

Query Match 100.0%; Score 501; DB 10; Length 731;  
Best Local Similarity 100.0%; Pred. No. 2.5e-35;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 VAAAKSAKVAKAQLRRAAGIGAGIGAGVGAGVGAGVGAGVGAGVGAGVGAG 60  
498 VAAAKSAKVAKAQLRRAAGIGAGIGAGVGAGVGAGVGAGVGAGVGAGVGAG 557  
Qy ADEGVRSLSPELRREGDSSSSQHLPTSPSPRVGALAAAK 101  
61 ADEGVRSLSPELRREGDSSSSQHLPTSPSPRVGALAAAK 101  
Qy ADEGVRSLSPELRREGDSSSSQHLPTSPSPRVGALAAAK 598  
558 ADEGVRSLSPELRREGDSSSSQHLPTSPSPRVGALAAAK 598

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RESULT 2
US-10-852-065-4
; Sequence 4, Application US/10852065
; Publication No. US20040253220A1
; GENERAL INFORMATION:
; APPLICANT: PERIER, Eric
; APPLICANT: CENIZO, Val,rie
; APPLICANT: BOUEZ, Charbel
; APPLICANT: SOMMER, Pascal
; APPLICANT: DAMOUR, Odile
; APPLICANT: GLEYZAL, Claudine
; APPLICANT: ANDRE, Val,rie
; APPLICANT: REYMERMIER, Corinne
; TITLE OF INVENTION: Stimulation of the synthesis and of the activity of an isoform
; TITLE OF INVENTION: of lysyl oxidase-like LOXL for stimulating the formation of
; FILE REFERENCE: 11123.81US01
; CURRENT APPLICATION NUMBER: US/10/852,065
; CURRENT FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: FR 03 07177
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 788
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-852-065-4

Query Match          97.8%; Score 490; DB 16; Length 788;
Best Local Similarity 98.1%; Pred. No. 2,4e-34;
Matches 101; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 VAAAKSAKVAAKQOLRAAGIGAGIPGLGVGVGPGIGVGAGVPGFGA- 59
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DB 553 VAAAKSAKVAAKQOLRAAGIGAGIPGLGVGVGPGIGVGAGVPGFGAV 612
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QY 60 -GADGVRRLSPELREGDPSSSOHLPTPSSPRVPGALAAK 101
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DB 613 PGADGVRRLSPELREGDPSSSOHLPTPSSPRVPGALAAK 655
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RESULT 3
US-10-852-575-3
; Sequence 3, Application US/10852575
; Publication No. US20040258676A1
; GENERAL INFORMATION:
; APPLICANT: PERIER, Eric
; APPLICANT: BOUEZ, Charbel
; APPLICANT: CENIZO, Valerie
; APPLICANT: SOMMER, Pascal
; APPLICANT: DAMOUR, Odile
; APPLICANT: GLEYZAL, Claudine
; APPLICANT: ANDRE, Valerie
; APPLICANT: REYMERMIER, Corinne
; APPLICANT: ORLY, Isabelle
; TITLE OF INVENTION: Stimulation of the activity of an isoform of lysyl oxidase
; TITLE OF INVENTION: for combating against some pathologies due to an incomplete,
; FILE REFERENCE: 11123.82US01
; CURRENT APPLICATION NUMBER: US/10/852,575
; CURRENT FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: FR 03 07178
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 788
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-852-575-3
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Query Match          97.8%; Score 490; DB 16; Length 788;
Best Local Similarity 98.1%; Pred. No. 2,4e-34;
Matches 101; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 VAAAKSAKVAAKQOLRAAGIGAGIPGLGVGVGPGIGVGAGVPGFGA- 59
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DB 553 VAAAKSAKVAAKQOLRAAGIGAGIPGLGVGVGPGIGVGAGVPGFGAV 612
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QY 60 -GADGVRRLSPELREGDPSSSOHLPTPSSPRVPGALAAK 101
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DB 613 PGADGVRRLSPELREGDPSSSOHLPTPSSPRVPGALAAK 655
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RESULT 4
US-10-104-047-2915
; Sequence 2915, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2915
; LENGTH: 617
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2915

Query Match          60.8%; Score 304.5; DB 15; Length 617;
Best Local Similarity 67.3%; Pred. No. 2,5e-18;
Matches 68; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 1 VAAAKSAKVAAKQOLRAAGIGAGIPGLGVGVGPGIGVGAGVPGFGA- 60
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DB 435 VAAAKSAKVAAKQOLRAAGIGAGIPGLGVGVGPGIGVGAGVPGFGA- 493
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QY 61 ADEGVRRLSPELREGDPSSSOHLPTPSSPRVPGALAAK 101
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DB 494 -----VPGALAAK 502
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RESULT 5
US-10-108-260A-2477
; Sequence 2477, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2477
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-2477

Query Match          60.8%; Score 304.5; DB 15; Length 663;
Best Local Similarity 67.3%; Pred. No. 2,7e-18;
Matches 68; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 1 VAAAKSAKVAAKQOLRAAGIGAGIPGLGVGVGPGIGVGAGVPGFGA- 60
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DB 463 VAAAKSAKVAAKQOLRAAGIGAGIPGLGVGVGPGIGVGAGVPGFGA- 521
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QY 61 ADEGVRRLSPELREGDPSSSOHLPTPSSPRVPGALAAK 101
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;; PRIOR FILING DATE: 2003-  
; NUMBER OF SEQ ID NOS: 31

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; SOFTWARE: Patentin version 3.2
; SEQ ID NO 27
; LENGTH: 244
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: silk and elastin peptide repeat sequence
US-10-845-775A-27

Query Match          30.7%; Score 154; DB 16; Length 244;
Best Local Similarity 45.7%; Pred. No. 1.2e-05;
Matches 42; Conservative 7; Mismatches 31; Indels 12; Gaps 4;

QY 3 AAKSAKVAAKQAQLRAAGLGGIPIGLGV-GVGVPGGLGV-----GAGVPGGLGV-GAGV 54
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 151 AGSGAGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAG 210
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 55 PGFGAGADGCVRRSLSPELREGDPSSSQHLPS 86
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 211 PGAGAGSGAGAGSGAGAGAM----DPGRYQDLRS 238

RESULT 12
US-10-845-936A-27
; Sequence 27, Application US/10845936A
; Publication No. US20040234609A1
; GENERAL INFORMATION:
; APPLICANT: Collier, Katherine D.
; APPLICANT: Cuevas, William A.
; APPLICANT: Kumar, Manoj A.
; TITLE OF INVENTION: Repeat Sequence Protein Polymer Active Agent Conjugates, Methods
; TITLE OF INVENTION: and Uses
; FILE REFERENCE: DOC0068BA/DC5058/GC792
; CURRENT APPLICATION NUMBER: US/10/845,936A
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: 60/470,464
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 27
; LENGTH: 244
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: silk and elastin peptide repeat sequence
US-10-845-936A-27

Query Match          30.7%; Score 154; DB 16; Length 244;
Best Local Similarity 45.7%; Pred. No. 1.2e-05;
Matches 42; Conservative 7; Mismatches 31; Indels 12; Gaps 4;

QY 3 AAKSAKVAAKQAQLRAAGLGGIPIGLGV-GVGVPGGLGV-----GAGVPGGLGV-GAGV 54
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 151 AGSGAGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAG 210
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 55 PGFGAGADGCVRRSLSPELREGDPSSSQHLPS 86
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 211 PGAGAGSGAGAGSGAGAGAM----DPGRYQDLRS 238

RESULT 13
US-10-939-036-27
; Sequence 27, Application US/10939036
; Publication No. US20050142094A1
; GENERAL INFORMATION:
; APPLICANT: Kumar, Manoj
; TITLE OF INVENTION: Use of Repeat Sequence Protein Polymers
; TITLE OF INVENTION: in Personal Care Compositions
; FILE REFERENCE: GC792-4-2
; CURRENT APPLICATION NUMBER: US/10/939,036
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 10/800,179
; PRIOR FILING DATE: 2004-03-12
```

```
; PRIOR APPLICATION NUMBER: US 60/454,077
; PRIOR FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 244
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: SELP-47K-3
US-10-939-036-27

Query Match          30.7%; Score 154; DB 18; Length 244;
Best Local Similarity 45.7%; Pred. No. 1.2e-05;
Matches 42; Conservative 7; Mismatches 31; Indels 12; Gaps 4;

QY 3 AAKSAKVAAKQAQLRAAGLGGIPIGLGV-GVGVPGGLGV-----GAGVPGGLGV-GAGV 54
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 151 AGSGAGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAG 210
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 55 PGFGAGADGCVRRSLSPELREGDPSSSQHLPS 86
   |||||:|:|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|
DB 211 PGAGAGSGAGAGSGAGAGAM----DPGRYQDLRS 238

RESULT 14
US-10-800-179-26
; Sequence 26, Application US/10800179
; Publication No. US20040180027A1
; GENERAL INFORMATION:
; APPLICANT: Cuevas, William A.
; APPLICANT: Kumar, Manoj
; TITLE OF INVENTION: Use of Repeat Sequence Protein Polymers in Personal Care
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: DOC 0057 PA / GC792-4 / DC 5074
; CURRENT APPLICATION NUMBER: US/10/800,179
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: 60/454,077
; PRIOR FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 26
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: SELP 47R-3
US-10-800-179-26

Query Match          30.7%; Score 154; DB 16; Length 246;
Best Local Similarity 45.7%; Pred. No. 1.2e-05;
Matches 42; Conservative 7; Mismatches 31; Indels 12; Gaps 4;

QY 3 AAKSAKVAAKQAQLRAAGLGGIPIGLGV-GVGVPGGLGV-----GAGVPGGLGV-GAGV 54
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 153 AGSGAGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAG 212
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 55 PGFGAGADGCVRRSLSPELREGDPSSSQHLPS 86
   |||||:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|
DB 213 PGAGAGSGAGAGSGAGAGAM----DPGRYQDLRS 240

RESULT 15
US-10-800-179-28
; Sequence 28, Application US/10800179
; Publication No. US20040180027A1
; GENERAL INFORMATION:
; APPLICANT: Cuevas, William A.
; APPLICANT: Kumar, Manoj
; TITLE OF INVENTION: Use of Repeat Sequence Protein Polymers in Personal Care
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: DOC 0057 PA / GC792-4 / DC 5074
; CURRENT APPLICATION NUMBER: US/10/800,179
```





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 10, 2005, 07:25:52 ; Search time 24.6219 Seconds  
(without alignments)  
394.685 Million cell updates/sec

Title: US-09-743-818A-4\_COPY\_500\_600

Perfect score: 501

Sequence: 1 VAAAKSAKAVAKAQLRAA.....QHLPSTPSPRPVGLAAAK 101

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501	100.0	792	1 EAHU	elastin precursor,
2	265	52.9	860	1 EAMS	elastin precursor
3	254.5	52.8	747	1 EABO	elastin precursor,
4	249.5	49.8	864	1 EART	elastin precursor
5	231	46.1	770	2 A59623	elastin precursor - she
6	154.5	30.8	784	2 A26601	elastin precursor
7	135.5	27.0	76	2 A5885	elastin - bovine (
8	130	25.9	907	2 A45560	sporozoite surface
9	117	23.4	1596	2 A33106	neurogenic locus m
10	112.5	22.5	127	2 E82734	hypothetical prote
11	109.5	21.9	505	2 T04143	CuBI protein - tom
12	109	21.0	532	2 T35119	probable aminotran
13	105	21.0	1329	2 T29074	hypothetical prote
14	104	20.8	151	2 T08002	glycine-rich prote
15	103.5	20.7	108	2 G86252	hypothetical prote
16	103.5	20.7	185	2 UC4085	glycine-rich cutic
17	103	20.6	100	2 T17558	glycine-rich prote
18	102.5	20.5	129	2 T17530	glycine-rich prote
19	100	20.0	419	2 G70602	hypothetical prote
20	99.5	19.9	130	2 T04048	hypothetical prote
21	99.5	19.9	1901	2 F70806	hypothetical glyci
22	99	19.8	108	2 S01844	fibroin - silkworm
23	99	19.8	447	2 G84687	probable disease r
24	98.5	19.7	158	2 T08957	glycine-rich prote
25	98.5	19.7	1240	2 T04193	hypothetical prote
26	98	19.6	143	2 S43071	hypothetical prote
27	98	19.6	1147	1 MMAX1B	myosin heavy chain
28	97.5	19.5	1733	1 B45344	probable nuclear a
29	97.5	19.5	1958	2 B40505	hypothetical prote

30	96.5	19.3	107	2 B85356	glycine-rich prote
31	96.5	19.3	149	2 T18758	hypothetical prote
32	96.5	19.3	554	1 P2WL41	I2 protein - human
33	96.5	19.3	671	2 A35912	homeotic protein o
34	96	19.2	162	2 C85356	glycine-rich prote
35	95.5	19.1	212	2 E86179	hypothetical prote
36	95	19.0	223	2 B96506	hypothetical prote
37	95	19.0	490	2 T09084	phosphatidylinosit
38	95	19.0	754	2 A55267	collagen alpha 5(I
39	95	19.0	1758	2 T29350	hypothetical prote
40	95	19.0	1759	2 T29351	collagen alpha 2(I
41	94.5	18.9	162	2 S56703	glycine-rich cell
42	94.5	18.9	171	2 T43959	hypothetical prote
43	94.5	18.9	459	2 T35317	probable serine/th
44	94.5	18.9	838	2 AC1064	outer membrane fin
45	94	18.8	208	2 S23463	cuticular protein

#### ALIGNMENTS

##### RESULT 1

EAHU  
elastin precursor, long splice form - human  
N:Alternate names: tropoelastin

C:Species: Homo sapiens (man)  
C>Date: 22-Jun-1990 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004

C/Accession: A32707; A33705; A30524; A53891

R:Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Sheppard, P.; Andersson, N.; Rosenblom, J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 5680-5684, 1987

A:Title: Alternative splicing of human elastin mRNA indicated by sequence analysis of c  
A:Reference number: A32707; MUID:87289668; PMID:3039501

A:Accession: A32707

A:Residues: 1-500,507-792 <IND>

A:Cross-references: UNIPROT:P15502; UNIPROT:Q9UMK5; GB:M16983; GB:U02948

R:Behar, M.M.; Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Rosenblom, J.C.; Abrams, W  
J. Biol. Chem. 264, 8887-8891, 1989

A:Title: Characterization of the complete human elastin gene. Delineation of unusual fe  
A:Reference number: A33705; MUID:89255358; PMID:2722804

A:Accession: A33705

A:Molecule type: DNA

A:Residues: 1-27 <BAS>

A:Cross-references: GB:J04821; NID:9182052; PIND:AA52379.1; PID:9553276  
R:Fazio, M.J.; Olsen, D.R.; Kaub, E.A.; Baldwin, C.T.; Indik, Z.; Ornstein-Goldstein, N

J. Invest. Dermatol. 91, 458-464, 1988

A:Title: Cloning of full-length elastin cDNAs from a human skin fibroblast recombinant  
A:Reference number: A30524; MUID:89009960; PMID:3171221

A:Accession: A30524

A:Molecule type: mRNA

A:Residues: 1-453,483-617,651-792 <FA2>

A:Cross-references: EMBL:M36860; NID:9182061; PIND:AA52382.1; PID:9182062  
R:Fazio, M.J.; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rosenblom, J.;

Lab. Invest. 58, 270-277, 1988

A:Title: Isolation and characterization of human elastin cDNAs, and age-associated var  
A:Reference number: A53891; MUID:88156138; PMID:2831431

A:Accession: A53891

A:Molecule type: mRNA

A:Residues: 164-453,483-500,507-617,651-792 <FA2>

A:Cross-references: GB:M24782; NID:9182063; PIND:AA53190.1; PID:9182064

C/Comment: The term tropoelastin refers to a soluble precursor form of the extracellula  
line oxidase activity.

C:Genetics:

A:Gene: GDB:ELN

A:Cross-references: GDB:119107; OMIM:130160

A:Map position: 7q11.23-7q11.23

C:Superfamily: elastin

C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine  
F.12-797/Product: elastin #status predicted <MAT>  
F.782-787/Dissulfide bonds: #status predicted

	Query Match	100.0%	Score 501:	DB 1:	Length 792:
	Best Local Similarity	100.0%	Pred. No. 4.2e-33:		
	Matches 101;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1 VAAAKSAKAAKAAKQLRRAAGLGGAGTGCGLGVGVGPGLGAGVPGLGAGVPBGCGAG	60			
Dd	559 VAAAKSAAKAAKAAKQLRRAAGLGGAGTGCGLGVGVGPGLGAGVPGLGAGVPBGCGAG	618			
Qy	61 ADEGVRRSLSPELREGDPPSSQHLLPSTPSSPRVPGALAAAK	101			
Dd	619 ADEGVRRSLSPELREGDPPSSQHLLPSTPSSPRVPGALAAAK	659			

RESULT 2

```

elastin precursor - mouse
N:Alternate names: tropoelastin
C:Species: Mus musculus (house mouse)
C>Date: 18-Aug-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: A55721
R:Wynder, K.S.; Seehler, J.L.; Boyd, C.D.; Passmore, H.C.
Genomics 23, 125-131, 1994
A>Title: Use of an intron length polymorphism to localize the tropoelastin gene to mouse
A:Reference number: A55721; PMID:95130069; PMID:7829060
A:Accession: A55721
A:Molecule type: mRNA
A:Residues: 1-860 <WVD>
A:Cross-references: UNIPROT:P54320; GB:U08210; NID:g473273; PIDN:AAA80155.1; PID:g473274
C:Genetics:
A:Map position: 5
A:Superfamily: elastin
C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxyllysine
F:1-27/Domains: signal sequence #status predicted <SIG>
F:28-860/Product: elastin #status predicted <MAT>
F:850-855/Disulfide Bonds: #status predicted

```

### RESULT 3

```

Query Match      52.9%; Score 265; DB 1; Length 860;
Best Local Similarity 60.6%; Pred. No. 4.4e-14;
Matches 60; Conservative 3; Mismatches 14; Indels 22; Gaps 3;

QY 3 AAASAAAVAAKAOULRAAAGAGAGPGLGVGVGVGAGVAGLVGAGVPGFGAGAD 62
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 592 AAASAAVAAKAOULRAAAGAGAGVPGFGAGAGVPGFGAGAGVPGFGAGAGVPGFGAGA - 650
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 63 EGVRRSLSPELREGDPSSQHLPTSPSSPRPGVGLAAAK 101
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 651 -GV-----PGFGAG-----AVPGSLAAASK 668
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

## EABO

elastin precursor, splice form a - bovine  
N.Alternate names: tropoelastin  
M.Contains: elastin precursor, splice form b; elastin precursor, splice form c  
C.Species: Bos primigenius taurus (cattle)  
C.Date: 08-Jun-1989 #sequence revision 26-Jul-1996 #text change 09-Jul-2004  
A.Accession: A31865; A26728; B26728; C26728; A23433; I45886  
R.Yeh, H.; Anderson, N.; Ornstein-Goldstein, N.; Bashir, M.M.; Rosenbloom, J.C.; Abrams,  
Biochemistry 28, 2365-2370, 1989  
A.Title: Structure of the bovine elastin gene and S1 nuclease analysis of alternative sp  
A.Reference number: A31865; MUID:89274159; PMID:2543440  
A.Accession: A31865  
A.Molecule type: DNA  
A.Residues: 1-27 <YEH>  
A.Cross-references: UNIPROT:P04985; UNIPROT:Q28101; GB:J02855; NID:g340504; PIDD:AAA3077  
R.Raju, K.; Anwar, R.A.,  
J.Biol. Chem. 262, 5755-5762, 1987  
A.Title: Primary structures of bovine elastin a, b, and c deduced from the sequences of  
A.Reference number: A92640; MUID:87194772; PMID:3032943  
A.Accession: A26728  
A.Molecule type: mRNA  
A.Residues: 1, 'RS', 4-11, 'E', 13-636, 'V', 638-747 <RAJ>  
A.Cross-references: GB:J02711; NID:g163019; PIDD:AAA30503.1; PIDD:g163020

A:Accession: B26728  
A:Molecule type: mRNA  
A:Residues: 1, 'RS', 4-11, 'E', 13-225, 240-636, 'V', 638-747 <RA2>  
A:Cross-references: GB:K03505; NID:g163025; PIDD:AAA30505.1; PID:g163026  
A:Accession: C26728  
A:Molecule type: mRNA  
A:Residues: 1, 'RS', 4-11, 'E', 13-225, 260-636, 'V', 638-747 <RA3>  
A:Cross-references: GB:K03506; NID:g163027; PIDD:AAA30506.1; PID:g163028  
R:Citlil, G.; May, M.; Omstein-Goldstein, N.; Indik, Z.; Morrow, S.; Yeh, H.S.; Rosenbl  
Biochemistry 22, 3075-3080, 1985  
A>Title: Structure of the 3' portion of the bovine elastin gene.  
A:Reference number: A22343; MUID:85280426; PMID:12932576

## A; Cross-

Lab. Invest. 51, 605-623, 1984  
A.Title: Biology of disease: Elastin: Relation of protein and gene structure to disease  
A.Reference number: 145885; MUID:8505254; PMID:6150137  
A.Accession: 145886  
A.Status: preliminary; translated from GB/EMBL/DBJ  
A.Molecule type: DNA  
A.Residues: 678-683, 685-747 <ROS>  
A.Cross-references: GB:M1898; MID:g163015; PIND:AA96417.1; PID:g163018  
R.Brown, P.L.; Mecham, U.; Tisdale, C.; Mecham, R.P.  
Biochem. Biophys. Res. Commun. 186, 549-555, 1992  
A.Title: The cysteine residues in the carboxy terminal domain of tropoelastin form an intramolecular disulfide bond  
A.Reference number: A58621; MUID:92337651; PMID:1532791  
A.Contents: annotation, disulfide bonds  
C.Comment: The term tropoelastin refers to a soluble precursor form of the extracellular matrix oxidase activity.  
C.Genetics:  
A.Introns: 634/3; 653/3; 676/3; 689/3; 707/3; 716/3; 733/3  
A.Note: the list of introns is incomplete  
C.Superfamily: elastin  
C.Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine  
F1-1-747/Product: elastin precursor, splice form a #status predicted <EPa>  
F1-1-225, 260-747/Product: elastin precursor, splice form c #status predicted <EPC>  
F1-1-225, 240-747/Product: elastin precursor, splice form b #status predicted <EPb>  
F1-1-26/Domain: signal sequence #status predicted <SIG>  
F1-27-747/Product: elastin #status predicted <Mat>  
F1-105, 109, 252, 271, 275, 324, 327, 400, 404, 407, 445, 448, 489, 493, 544, 548, 552, 606, 609, 645, 649, 654, 657, 742/Disulfide Bonds: #status experimental

D**b**

Query Match	52.8%	Score 264.5;	DB 1;	Length 747;
Best Local Similarity	59.4%;	Pred. 4.2e-14;		
Matches	60;	Conservative 1;	Mismatches 7;	Indels 33; Gaps 1;
QY	1 VAAAKSAKAYAAATOLRAAAGLGAGTGGGVGVPGLGVGAAGVPGIGVGAAGVPGFGAG	60		
Dd	539 VPAAKSAAKAAAQAQFPAAAGLPAAGVGAVGAGVGLGVGAAGVPGILGVGAAGVPGFPGA	- 597		
QY	61 ADEGVRSLSPELTREDDPSSSGHLPTSPSSPRVYGALAAAK	101		
Dd	598 -----VGTLAAAK	606		

## RESULT 4

EART  
elastin precursor - rat  
N:Alternate names: tropoelastin  
C:Species: Rattus norvegicus (Norway rat)  
C.Date: 11-Jan-1991 #sequence revision 16-Aug-1996 #text change 09-Jul-2004  
C.Accession: A36106; A30878; J36523; S02173; I54172; I68505  
R:Pierce, R.A.; Deak, S.B.; Stoltie, C.A.; Boyd, C.D.  
Biochemistry 29, 9677-9683, 1990  
A>Title: Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning.  
A.Reference number: A36106; MUID:91104868; PMID:1702999  
A.Accession: A36106  
A:Molecule type: mRNA  
A:Residues: 1-864 <PIE>  
A:Cross-references: UNIPROT:Q09372; GB:M60647; GB:J05292; NID:G207444; PIDN:AAA42269.1;

R;Deak, S.B.; Pierce, R.A.; Belisky, S.A.; Riley, D.J.; Boyd, C.D.  
 J. Biol. Chem. 263, 13504-13507, 1988  
 A;Title: Rat tropoelastin is synthesized from a 3.5-kilobase mRNA.  
 A;Reference number: A30878; MUID:88330868; PMID:2971041  
 A;Accession: A30878  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 781-864 <DEA>  
 A;Cross-references: GB:U04035, NID:G207442, PIDN:AAA42268.1, PID:G207443  
 R;Franzblau, C.; Pratt, C.A.; Paris, B.; Colaninno, N.M.; Offner, G.D.; Mowayzel Jr., P.  
 J. Biol. Chem. 264, 15115-15119, 1989  
 A;Title: Role of tropoelastin fragmentation in elastogenesis in rat smooth muscle cells.  
 A;Reference number: A36523; MUID:89359327; PMID:2768256  
 A;Accession: A36523  
 A;Molecule type: protein  
 A;Residues: 22-31 <PRA>  
 R;Rich, C.B.; Foster, J.A.  
 Arch. Biochem. Biophys. 268, 551-558, 1989  
 A;Title: Characterization of rat heart tropoelastin.  
 A;Reference number: 502173; MUID:89117149; PMID:2913947  
 A;Accession: 502173  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1P, 369-545, 548-764, 770-864 <RIC>  
 A;Experimental source: heart  
 R;Pierce, R.A.; Alatawi, A.; Deak, S.B.; Boyd, C.D.  
 Genomics 12, 651-658, 1992  
 A;Title: Elements of the rat tropoelastin gene associated with alternative splicing.  
 A;Reference number: 154172; MUID:92241859; PMID:1572637  
 A;Accession: 154172  
 A;Status: translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 264-533 <RES>  
 A;Cross-references: GB:M86372; NID:G207455; PIDN:AAA42271.1; PID:G554527  
 A;Accession: 168505  
 A;Status: translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 558-864 <RE2>  
 A;Cross-references: GB:M86376; NID:G207459; PIDN:AAA42272.1; PID:G207462  
 C;Genetics:  
 A;Insertions: 277/1; 292/1; 308/1; 339/1; 359/1; 419/1; 437/1; 467/1; 484/1; 601/1; 621/1;  
 A;Notes: the list of introns may be incomplete  
 C;Superfamily: elastin  
 C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxyllysine  
 F;1-21/Domain: signal sequence #status predicted <SIG>  
 F;22-864/Product: elastin #status predicted <MAT>  
 F;854-859/Disulfide bonds: #status predicted

Query Match 49.8%; Score 249.5; DB 1; Length 864;  
 Best Local Similarity 56.6%; Pred. No. 7.8e-13;  
 Matches 56; Conservative 3; Mismatches 7; Indels 33; Gaps 2;

QY 3 AAKSAKVAKQQLRAAGAGIGPGAGVGPGLGVGAGVPGGLGVGAGVPGFGAGAD 62  
 DB 606 AAKSAKVAKQQLRAAGAGIGPGAGVGPGLGVGAGVPGFGAGAG--GFGAGAGVPGFGAGA- 662

QY 63 EGVRRSLSPRLREGDPSSQHLPTSPSPRVPGALAAK 101  
 DB 663 -----VPGSLAAAK 671

RESULT 5  
 S59623  
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C;Date: 23-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
 C;Accession: S59623; A24758  
 R;Muech, U.C.; Sandberg, L.B.; Roos, P.J.; Jimenez, F.; Christiano, A.M.; Deak, S.B.; Bo  
 Matrix Biol. 14, 635-641, 1994  
 A;Title: Extensive alternate exon usage at the 5' end of the sheep tropoelastin gene.  
 A;Reference number: S59623  
 A;Accession: S59623  
 A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA  
 A;Residues: 1-770 <MAU>  
 A;Cross-references: UNIPROT:P11547  
 R;Toon, K.; Davidson, J.M.; Boyd, C.; May, M.; LuValle, P.; Ornstein-Goldstein, N.; Smi  
 Arch. Biochem. Biophys. 241, 684-691, 1985  
 A;Title: Analysis of the 3' region of the sheep elastin gene.  
 A;Reference number: A24758; MUID:85305763; PMID:3839997  
 A;Accession: A24758  
 A;Molecule type: mRNA  
 A;Residues: 655-669, 671-716, 732-770 <YOO>  
 C;Superfamily: elastin  
 C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxyllysine  
 F;760-765/Disulfide bonds: #status predicted

Query Match 46.1%; Score 231; DB 2; Length 770;  
 Best Local Similarity 54.3%; Pred. No. 2.2e-11;  
 Matches 63; Conservative 6; Mismatches 17; Indels 30; Gaps 6;

QY 3 AAKSAKVAKQQLRAAGAGIGPGAGVGPGLGVGAGVPGFGAGVPGF----- 57  
 DB 549 AAKSAKVAKQQLRAAGAGIGPGAGVGPGLGVGAGVPGFGAGAG-VGTTLAAK 607

QY 58 -----GAGADGVRRLSPRLREGDPSSQHLPTSPSPRVPGALAAK 101  
 DB 608 AAKFAPGVGALGV-----GDLGGA-GIPGVGGVGPAAAL-GAKAAK 651

RESULT 6  
 A26601  
 A;Title: Repeating structure of chick tropoelastin revealed by complementary DNA cloning  
 A;Reference number: A26601; MUID:87242320; PMID:3593675  
 A;Accession: A26601  
 A;Molecule type: mRNA  
 A;Residues: 1-212, 237-524, 535-784 <BR2>  
 A;Cross-references: UNIPROT:P07916; GB:M15889; NID:G212803; PIDN:AAA49108.1; PID:G21280  
 R;Tokimitsu, I.; Tajima, S.; Nishikawa, T.; Tajima, W.; Fukasawa, T.  
 Arch. Biochem. Biophys. 256, 455-461, 1987  
 A;Title: Sequence analysis of elastin cDNA from chick aorta and tissue-specific transcr  
 A;Reference number: A27264; MUID:87297534; PMID:3502711  
 A;Accession: A27264  
 A;Molecule type: mRNA  
 A;Residues: 491-569, 'G', 571-604, 'A', 606-643, 'A', 645-667, 'R', 689-700, 'R', 702-784 <TOK>  
 A;Cross-references: GB:M18633; NID:G211742; PIDN:AAA48761.1; PID:G211743  
 C;Superfamily: elastin  
 C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxyllysine  
 F;1-24/Domain: signal sequence (fragment) #status predicted <SIG>  
 F;25-212, 237-524, 535-784/Product: elastin #status predicted <MAT>  
 F;773-779/Disulfide bonds: #status predicted

Query Match 30.8%; Score 154.5; DB 2; Length 784;  
 Best Local Similarity 45.7%; Pred. No. 3.1e-05;  
 Matches 53; Conservative 7; Mismatches 25; Indels 31; Gaps 9;

QY 2 AAKSAKVAKQQLRAAGAGIGPGAGVGPGLGVGAGVPGFGAGVPGF----- 48  
 DB 447 AAKSAKVAKQQLRAAGAGIGPGAGVGPGLGVGAGVPGFGAGAG-VGTTLAAK 506

QY 49 GV-GAGVPGFAGADGVRRLSPRLREGDPSSQHLPTSPSPRVPGALAAK 101



A;CROSS-References: UNIPROT:Q86525; EMBL:AL031124; NID:e1312893; PID:e1312918; PIDN:CA...

Query Match 20.7%; Score 103.5; DB 2; Length 108;

Best Local Similarity 49.08; Pred. No. 0.067;



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OM protein - protein search, using sw model

Run on: August 10, 2005, 07:17:42 ; Search time 113.06 Seconds  
(without alignments)  
457,457 Million cell updates/sec

Title: US-09-743-818a-4\_COPY\_500\_600

Perfect score: 501  
Sequence: 1 VAAAKSAKVAKAKQIRRA.....QHLPSTPSRPVGAALAAK 101

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501	100.0	757	2	Q14234
2	501	100.0	757	2	Q75W05
3	493	98.4	635	2	O15336
4	304.5	60.8	258	2	Q9UMF5
5	304.5	60.8	643	2	Q8NB14
6	304.5	60.8	687	2	O14235
7	304.5	60.8	687	2	Q72316
8	304.5	60.8	711	2	Q723F5
9	303.5	60.8	730	1	E1S_HUMAN
10	303.5	60.6	570	2	Q6ZM6
11	300.5	60.0	472	2	O8N2G0
12	296.5	59.2	602	2	O15337
13	274.5	54.8	650	2	Q28099
14	274.5	54.8	666	2	Q28096
15	274.5	54.8	707	2	Q28098
16	269	53.7	679	2	Q28097
17	265	52.9	810	2	Q9E829
18	265	52.9	860	1	E1S_MOUSE
19	265	52.9	860	1	Q8C9L8
20	264.5	52.8	747	1	E1S_BOVIN
21	249.5	49.8	864	1	E1S_RAT
22	219.5	43.8	658	1	Q6P0L4
23	152.5	30.4	750	1	E1S_CHICK
24	142.5	28.4	1092	2	Q967R2
25	142	28.3	553	2	Q6ZUN2
26	132	26.3	279	2	Q6C3L2
27	130	25.9	907	2	Q26675
28	122	24.4	194	2	Q6PY85
29	121.5	24.3	723	2	Q9NJ07
30	117.5	23.5	897	2	Q6O294
31	117	23.4	137	2	Q9GQX7

## ALIGNMENTS

32	117	23.4	196	2	Q8PZF2	Q8PZF2 methanogarc
33	117	23.4	205	2	Q25946	Q25946 plasmodium
34	117	23.4	239	2	Q6Z2M1	Q6Z2M1 oryza sativ
35	117	23.4	1594	2	Q9V6W7	Q9V6W7 drosophila
36	117	23.4	1596	1	MAM_DROME	P21519 drosophila
37	114	22.8	5263	1	FBOH_BOMMO	P05790 bombyx mori
38	113	22.6	76	2	Q28100	Q28100 bos taurus
39	112.5	22.5	127	2	Q9PEK3	Q9PEK3 xylella fas
40	112.5	22.5	251	2	Q984T2	Q984T2 rhizobium 1
41	112.5	22.5	912	2	Q9B1T2	Q9B1T2 plectreureys
42	112	22.4	301	2	Q01927	Q01927 phytophthor
43	111.5	22.3	103	2	Q7Z5D6	Q7Z5D6 homo sapien
44	111	22.2	156	2	Q9GQX6	Q9GQX6 plasmodium
45	111	22.2	343	2	Q01914	Q01914 phytophthor

## RESULT 1

Q14234	PRELIMINARY;	PRT;	757 AA.
ID Q14234			
AC Q14234			
DT 01-NOV-1996 (TREMREL. 01, Created)			
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)			
DT 01-MAR-2004 (TREMREL. 26, Last annotation update)			
DE Elastin.			
GN Name=E1N;			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=87274906; PubMed=3038460;			
RA Indik Z., Yoon K., Morrow S.D., Cicilia G., Rosenbloom J.,			
RA Rosenbloom U., Ornstein-Goldstein N.,			
RT "Structure of the 3' region of the human elastin gene: great abundance			
RT of Alu repetitive sequences and few coding sequences."			
RL Connect. Tissue Res. 16:197-211(1987).			
DR EMBL; M17282; AAC98395.1; -			
DR EMBL; M16983; AAC98395.1; JOINED.			
DR EMBL; M17265; AAC98395.1; JOINED.			
DR EMBL; M17265; AAC98395.1; JOINED.			
DR EMBL; M17267; AAC98395.1; JOINED.			
DR EMBL; M17268; AAC98395.1; JOINED.			
DR EMBL; M17270; AAC98395.1; JOINED.			
DR EMBL; M17271; AAC98395.1; JOINED.			
DR EMBL; M17272; AAC98395.1; JOINED.			
DR EMBL; M17273; AAC98395.1; JOINED.			
DR EMBL; M17274; AAC98395.1; JOINED.			
DR EMBL; M17275; AAC98395.1; JOINED.			
DR EMBL; M17276; AAC98395.1; JOINED.			
DR EMBL; M17277; AAC98395.1; JOINED.			
DR EMBL; M17278; AAC98395.1; JOINED.			
DR EMBL; M17279; AAC98395.1; JOINED.			
DR EMBL; M17280; AAC98395.1; JOINED.			
DR EMBL; M17281; AAC98395.1; JOINED.			
GO; GO:0005578; C:extracellular matrix (sensu Metazoa); NAS.			
GO; GO:0030023; F:extracellular matrix constituent conferring. . .; NAS.			
DR InterPro; IPR001451; Hexapep_cranst.			
DR InterPro; IPR003979; tropoelastin.			
DR PRINTS; PR01500; TROP0ELASTIN.			
DR PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.			
SEQUENCE 757 AA; 66136 MW; 2387P55B8AP55C8_CRC64;			

Query Match 100.0%; Score 501; DB 2; Length 757;  
Best Local Similarity 100.0%; Pred. No. 8.6e-28;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAAAKSAKVAKAAQLRRAAGIGAGIPGLGVGVGPGIGVAGVPGIGVAGVPGFGAG 60  
|||||  
DB 524 VAAAKSAKVAKAAQLRRAAGIGAGIPGLGVGVGPGIGVAGVPGIGVAGVPGFGAG 583  
|||||

QY 61 ADEGVRSLSPELREDPSSQHLPTSPSPRPVPGALAAK 101  
|||||  
DB 584 ADEGVRSLSPELREDPSSQHLPTSPSPRPVPGALAAK 624  
|||||

RESULT 2  
ID Q9UMF5 PRELIMINARY; PRT; 757 AA.  
AC Q95W05;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein ELN.  
GN Name=ELN;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;  
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,  
Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,  
Wyllie G.A., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,  
Fewell G.A., Delehaunty K.D., Miner T.L., Naeh W.E., Cordes M., Du H.,  
Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,  
Vandbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,  
Ozeraky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,  
Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,  
Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,  
Tin-Mollam A.M., Abbott A., Mink P., Maupin R., Strommatt C.,  
Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,  
Wendt M.C., Yang S.P., Schultz B.R., Wallis J.W., Spielh J.,  
Bieri T.A., Nelson J.O., Berkowicz N., Wohlmann P.E., Cook L.L.,  
Hickobotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,  
Clifton S.W., Chisoe S.L., Marra M.A., Raymond C., Haugen E.,  
Gillert W., Zhou Y., James R., Phelps K., Iadonoto S., Bub K.,  
Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,  
Baerisch R.A., Brent M.R., Keibler E., Filcek P., Bork P., Suyama M.,  
Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Ghosh W.R.,  
Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,  
Waterston R.H., Wilson R.K.;  
RT "The DNA sequence of human chromosome 7.";  
RL Nature 424:157-164(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Waterston R.;  
RN Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Wilson R.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC005056; AA007435.1; -;  
DR GO; GO:0005578; Extracellular matrix (sensu Metazoa); IEA.  
DR GO; GO:0005201; Extracellular matrix structural constituent, IEA.  
DR InterPro; IPR001451; Hexapep\_cristin.  
DR PRINTS; PR01500; TROPOLASTIN.  
DR PROSITE; PS00101; HEXAPEP\_TRANSFERRASES; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 757 AA; 66106 MW; 2B24F955D8360738 CRC64;

Query Match 100.0%; Score 501; DB 2; Length 757;  
Best Local Similarity 100.0%; Pred. No. 8.6e-28;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAAAKSAKVAKAAQLRRAAGIGAGIPGLGVGVGPGIGVAGVPGIGVAGVPGFGAG 60  
|||||  
DB 524 VAAAKSAKVAKAAQLRRAAGIGAGIPGLGVGVGPGIGVAGVPGIGVAGVPGFGAG 583  
|||||

QY 61 ADEGVRSLSPELREDPSSQHLPTSPSPRPVPGALAAK 101  
|||||  
DB 584 ADEGVRSLSPELREDPSSQHLPTSPSPRPVPGALAAK 624  
|||||

RESULT 3  
ID O15336 PRELIMINARY; PRT; 635 AA.  
AC O15336;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Elastin (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97358574; PubMed=9215670; DOI=10.1093/hmg/6.7.1021;  
RA Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,  
Morris C.A., Keating M.T.;  
RT "Elastin point mutations cause an obstructive vascular disease,  
supravalvular aortic stenosis.";  
RL Hum. Mol. Genet. 6:1021-1028(1997).  
DR EMBL; U93037; AAB65621.1; JOINED.  
DR EMBL; U93034; AAB65621.1; JOINED.  
DR EMBL; U93035; AAB65621.1; JOINED.  
DR EMBL; U93036; AAB65621.1; JOINED.  
GO; GO:0005578; Extracellular matrix (sensu Metazoa); IEA.  
DR GO; GO:0005201; Extracellular matrix structural constituent, IEA.  
DR InterPro; IPR001451; Hexapep\_transf.  
DR PRINTS; PR01500; TROPOLASTIN.  
DR PROSITE; PS00101; HEXAPEP\_TRANSFERRASES; UNKNOWN\_1.  
FT NON TER 1  
FT NON TER 635  
FT NON TER 635  
SQ SEQUENCE 635 AA; 55279 MW; 72950C36412782A4 CRC64;

Query Match 98.4%; Score 493; DB 2; Length 635;  
Best Local Similarity 99.0%; Pred. No. 2.7e-27;  
Matches 100; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VAAAKSAKVAKAAQLRRAAGIGAGIPGLGVGVGPGIGVAGVPGIGVAGVPGFGAG 60  
|||||  
DB 531 VAAAKSAKVAKAAQLRRAAGIGAGIPGLGVGVGPGIGVAGVPGIGVAGVPGFGAG 590  
|||||

QY 61 ADEGVRSLSPELREDPSSQHLPTSPSPRPVPGALAAK 101  
|||||  
DB 591 ADEGVRSLSPELREDPSSQHLPTSPSPRPVPGALAAK 631  
|||||

RESULT 4  
ID Q9UMF5 PRELIMINARY; PRT; 258 AA.  
AC Q9UMF5;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Elastin (Fragment).  
GN Name=ELN;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.



RX	MEDLINE=96411691; PubMed=8812460; DOI=10.1006/geno.1996.0469;
RA	Osborne L.R., Mattindale D.W., Scherer S.W., Shi X.-M., Huizenga J.,
RA	Heng H.H.Q., Costa T., Robber B., Lew L., Brinkman J., Rommens J.,
RT	"Comparative genomic sequence analysis of the Williams syndrome region
RT	commonly deleted in Williams syndrome patients.";
RL	Genomics 36:328-336(1996).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20458686; PubMed=11003705;
RA	Mattindale D.W., Wilson M.D., Wang D., Burke R.D., Chen X.,
RA	Duronio V., Koop B.F.;
RT	"Comparative genomic sequence analysis of the Williams syndrome region
RT	(LIMK1-RFC2) of human chromosome 7q11.23.";
RL	Mamm. Genome 11:890-898(2000).
DR	EMBL; U63721; AACI384.1; -.
DR	InterPro; IPR001451; Hexaprep_transf.
DR	PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
FT	NON TER
SQ	SEQUENCE 258 AA; 21990 MW; C39BF7298D0B5D2 CRC64;
Query Match	60.8%; Score 304.5; DB 2; Length 258;
Best Local Similarity	67.3%; Pred. No. 2.9e-14;
Matches 68; Conservative 0; Mismatches 0; Indels 33; Gaps 1;	
QY	1 VAAAKSAKVAAKQLRAAAGLGAGTGTGCGVGVPGVLGGAGVPGLGVGAGVPGFGAG 60 
DB	58 VAAAKSAKVAAKQLRAAAGLGAGTGTGCGVGVPGVLGGAGVPGLGVGAGVPGFGA- 116 
QY	61 ADEGVRRSLSPELREGDPSSSQHLPTSTPSSPVGPALAAK 101 
DB	117 -----VPGALAAAK 125 
RESULT 5	
OSNB14	PRELIMINARY; PRT; 643 AA.
ID	OSNB14
AC	OSNB14;
DT	01-OCT-2002 (TREMBLrel. 22, Created)
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE	Hypothetical protein PSEC0254.
OC	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Euteria; Primates; Catarrhini; Homidae; Homo.
OX	NCBI_TaxId=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Ota T., Mishikawa T., Suzuki Y., Kawai-Hiro Y., Hayaishi K., Ishii S.,
RA	Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA	Nagahara K., Sugano S., Isozaki T.;
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AK075554; BA011696.1; -.
DR	HSSP; P50099; 1ZRF.
DR	GO; GO:0005576; Cytoplasmic matrix (sensu Metazoa); IEA.
DR	GO; GO:0005201; Extracellular matrix structural constituent; IEA.
DR	InterPro; IPR001451; Hexapep_transf.
DR	InterPro; IPR003979; tropoelectin.
DR	PRINTS; PR01500; TROPOELASTIN.
DR	PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
SQ	SEQUENCE 643 AA; 55629 MW; FDP0C4261E72A69 CRC64;
Query Match	60.8%; Score 304.5; DB 2; Length 643;
Best Local Similarity	67.3%; Pred. No. 6.3e-14;
Matches 68; Conservative 0; Mismatches 0; Indels 33; Gaps 1;	
QY	1 VAAAKSAKVAAKQLRAAAGLGAGTGTGCGVGVPGVLGGAGVPGLGVGAGVPGFGAG 60 
DB	443 VAAAKSAKVAAKQLRAAAGLGAGTGTGCGVGVPGVLGGAGVPGLGVGAGVPGFGA- 501 
QY	61 ADEGVRRSLSPELREGDPSSSQHLPTSTPSSPVGPALAAK 101 
DB	502 -----VPGALAAAK 510 

```

RESULT 6
ID 014235 PRELIMINARY; PRT; 687 AA.
AC 014235;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Blastin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87289668; PubMed=3038460;
RA Indik Z., Yoon K., Morrow S.D., Gicila G., Rosenbloom J.,
RA Rosenbloom U., Ornstein-Goldstein N.;
RT "Structure of the 3' region of the human elastin gene: great abundance
RT of Alu repetitive sequences and few coding sequences.";
RL Connect. Tissue Res. 16:197-211(1987).
DR EMBL; M17282; AAC98393.1; JOINED.
DR EMBL; M16983; AAC98393.1; JOINED.
DR EMBL; M17265; AAC98393.1; JOINED.
DR EMBL; M17266; AAC98393.1; JOINED.
DR EMBL; M17267; AAC98393.1; JOINED.
DR EMBL; M17268; AAC98393.1; JOINED.
DR EMBL; M17271; AAC98393.1; JOINED.
DR EMBL; M17272; AAC98393.1; JOINED.
DR EMBL; M17273; AAC98393.1; JOINED.
DR EMBL; M17275; AAC98393.1; JOINED.
DR EMBL; M17276; AAC98393.1; JOINED.
DR EMBL; M17277; AAC98393.1; JOINED.
DR EMBL; M17278; AAC98393.1; JOINED.
DR EMBL; M17279; AAC98393.1; JOINED.
DR EMBL; M17281; AAC98393.1; JOINED.
DR HSBP; P50099; 12FU.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); NAS.
DR GO; GO:0030023; F:extracellular matrix constituent conferring. . .; NAS.
DR InterPro; IPR001455; Hexapep_transf.
DR InterPro; IPR003979; Tropoelastin.
DR PRINTS; PRO1500; TROPOELASTIN.
DR PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
SQ SEQUENCE 687 AA; 59525 MW; 864068C4C8E9F88F CRC64;

Query Match 60.8%; Score 304.5; DB 2; Length 687;
Best Local Similarity 67.3%; Pred. No. 6,6e-14;
Matches 68; Conservative 0; Mismatches 0; Indels 33; Gaps 1

QY 1 VAAAAAQAQVAAKQAOLRAAGIGAGIPGLGVGVPGIGVAGVPGIGAGVPGFGAG 60
DB 505 VAAASAAVAAKQAOLRAAGIGAGIPGLGVGVPGIGVAGVPGIGAGVPGFGA 565
QY 61 ADEGVRSLSPELRGDPSSSOHLDPSTPSSPRVPCALAAK 101
DB 564 -----VPGALAAK 572

RESULT 7
ID 072316 PRELIMINARY; PRT; 687 AA.
AC 072316;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)

```



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CC Comment-Additional isoforms seem to exist;
CC Name=1;
CC IsoId=PI5502-1; Sequence=Displayed;
CC Name=2;
CC IsoId=PI5502-2; Sequence=VSD_004243;
CC -1- PTM: The crosslinks are made of deaminated Lys.
CC -1- DISEAS: Defects in ELN are a cause of autosomal dominant cutis
CC laxa [MIM:123700]. Cutis laxa is a rare connective tissue disorder
CC characterized by loose, hyperextensible skin with decreased
CC resiliency and elasticity leading to a premature aged appearance.
CC The skin changes are often accompanied by extracutaneous
CC manifestations, including pulmonary emphysema, bladder
CC diverticula, pulmonary artery stenosis and pyloric stenosis.
CC -1- DISEAS: Haploinsufficiency of ELN may be the cause of certain
CC cardiovascular and musculo-skeletal abnormalities observed in
CC Williams-Beuren syndrome (WBS) [MIM:194050]. WBS is a rare
CC developmental disorder and a contiguous gene deletion syndrome
CC involving genes from chromosome band 7q11.23.
CC -1- DISEAS: Defects in ELN are the cause of supravalvular aortic
CC stenosis (SVAS) [MIM:185500]. SVAS is a congenital narrowing of
CC the ascending aorta which can occur sporadically, as an autosomal
CC dominant condition, or as one component of Williams-Beuren
CC syndrome.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@ib-sib.ch).
CC -----
DR EMBL, M17282; AAC98394.1; JOINED.
DR EMBL, M16983; AAC98394.1; JOINED.
DR EMBL, M17265; AAC98394.1; JOINED.
DR EMBL, M17266; AAC98394.1; JOINED.
DR EMBL, M17267; AAC98394.1; JOINED.
DR EMBL, M17268; AAC98394.1; JOINED.
DR EMBL, M17270; AAC98394.1; JOINED.
DR EMBL, M17271; AAC98394.1; JOINED.
DR EMBL, M17272; AAC98394.1; JOINED.
DR EMBL, M17273; AAC98394.1; JOINED.
DR EMBL, M17275; AAC98394.1; JOINED.
DR EMBL, M17276; AAC98394.1; JOINED.
DR EMBL, M17277; AAC98394.1; JOINED.
DR EMBL, M17278; AAC98394.1; JOINED.
DR EMBL, M17279; AAC98394.1; JOINED.
DR EMBL, M17280; AAC98394.1; JOINED.
DR EMBL, M17281; AAC98394.1; JOINED.
DR EMBL, M36660; AAA52382.1; -.
DR EMBL, M24782; AAA53190.1; -.
DR EMBL, U62292; AAB17544.1; -.
DR EMBL, X15603; CAA33627.1; -.
DR PIR, A32707; BAHU.
DR HSSP, P50099; IZFU.
DR Genew; HGNC:3327; ELN.
DR MIM, 130160; -.
DR MIM, 123700; -.
DR MIM, 194050; -.
DR MIM, 185500; -.
DR GO, GO:0005578; C:extracellular matrix; TAS.
DR GO, GO:0005615; C:extracellular space; TAS.
DR GO, GO:0005201; F:extracellular matrix structural constituent; TAS.
DR GO, GO:0008283; P:cell proliferation; TAS.
DR GO, GO:0008015; P:circulation; TAS.
DR GO, GO:0009887; P:organogenesis; TAS.
DR GO, GO:0007585; P:respiratory gaseous exchange; TAS.
DR InterPro, IPR003979; trpocoe1astin.
DR PRINTS, PR01500; TROPOLASTIN.
DR Alternative splicing; Repeat; signal; structural protein;
KW Williams-Beuren syndrome.
FT SIGNAL 1 26
FT CHAIN 27 730 Elastin.

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FT	DISULFID	720	725	By similarity.
FT	VASAPLIC	472	477	Missing (in Isoform 2).
FT				/Ftrd:VSP 004243.
SQL	SEQUENCE	730 AA;	63260 MW;	AB06015B:567A:56 CRC64;
	Query Match	60.8%;	Score 304.5;	DB 1; Length 730;
	Best Local Similarity	67.3%;	Pred. No. 7e-14;	
	Matches	68;	Conservative	0; Mismatches 0; Indels 33; Gaps 1;
QY	1	VAAAKSAAKYAAQAQLRAAAGLGAGTIPGLGVGVGVGLGVGAAGVPGGLGVGAGVPGGAG	60	
DB	530	VAAAKSAAKYAAQAQLRAAAGLGAGTIPGLGVGVGVGLGVGAAGVPGGLGVGAGVPGGAG	588	
QY	61	ADEGVRRSLSPELAREGDPSSSQHLPSRPSPRVPGALAAK	101	
DB	589	-----VFGALAAAK	597	
	RESULT 10			
	Q6ZMJ6	PRELIMINARY;	PRT;	570 AA.
AC	Q6ZMJ6;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	Hypothetical protein FLJ16246.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.			
NC	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,			
RA	Wakabe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,			
RA	Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,			
RA	Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,			
RA	Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,			
RA	Wagatsuma M., Murakawa K., Kanehori Y., Takahashi-Fujii A., Oshima A.,			
RA	Masuhito Y., Nagai K., Isogai T.;			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AK122731; BAC85506.1; -			
DR	GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.			
DR	GO; GO:0005201; F:extracellular matrix structural constituent; IEA.			
DR	InterPro; IPR001451; Hexapep.transf.			
DR	InterPro; IPR003979; troponin.transf.			
DR	PRINTS; PR01500; TROPOELASTIN.			
DR	PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.			
SQL	SEQUENCE	570 AA;	48941 MW;	3117B02B:06054F:B CRC64;
	Query Match	60.6%;	Score 303.5;	DB 2; Length 570;
	Best Local Similarity	66.3%;	Pred. No. 6.7e-14;	
	Matches	67;	Conservative	1; Mismatches 0; Indels 33; Gaps 1;
QY	1	VAAAKSAAKYAAQAQLRAAAGLGAGTIPGLGVGVGVGLGVGAAGVPGGLGVGAGVPGGAG	60	
DB	388	VAAAKSAAKYAAQAQLRAAAGLGAGTIPGLGVGVGVGLGVGAAGVPGGLGVGAGVPGGAG	446	
QY	61	ADEGVRRSLSPELAREGDPSSSQHLPSRPSPRVPGALAAK	101	
DB	447	-----VFGALAAAK	455	
	RESULT 11			
	Q8N2G0	PRELIMINARY;	PRT;	472 AA.
AC	Q8N2G0;			
DT	01-OCT-2002 (TREMBLrel. 22, Created)			
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Hypothetical protein PSEC0191.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole embryo; Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Ota T., Nishikawa T., Wakamatsu A., Nagai T., Nakamura Y.,
RA Saito K., Yamamoto J., Isogai T.,
RA Nagahara K., Sugano S.,
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074949; BAC11651.1; -
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR001451; Hexapep_transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERSSES; UNKNOWN_1.
FT NON_TER 472 472
SQ SEQUENCE 472 AA; 42265 MW; 8D7A0F3A9BP971F3 CRC64;

Query Match 60.0%; Score 300.5; DB 2; Length 472;
Best Local Similarity 66.3%; Pred. No. 9.3e-14;
Matches 67; Conservative 0; Mismatches 1; Indels 33; Gaps 1;

OY 1 VAAAKSAKVAKAQOLRAAAGIGAGIPGLGVGVPGIGVAGVPGIGVAGVPGFGAG 60
DB 298 VAAAKSAKVAKAQOLRAAAGIGAGIPGLGVGVPGIGVAGVPGIGVAGVPGFGA- 356

OY 61 ADEGVRSLSPELREBDPSSSCHLPSTPSSPRVPGALAAK 101
DB 357 -----VPGALAAK 365

RESULT 12
ID 015337 PRELIMINARY; PRT; 602 AA.
AC 015337;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Elastin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97358574; PubMed=9215670; DOI=10.1093/hmg/6.7.1021;
RA Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,
RA Morris C.A., Keating M.T.;
RT "Elastin point mutations cause an obstructive vascular disease,
RT supravalvular aortic stenosis."
RL Hum. Mol. Genet. 6:1021-1028(1997).
DR EMBL; U93037; AAB5620.1; -
DR EMBL; U93037; AAB5620.1; JOINED.
DR EMBL; U93034; AAB5620.1; JOINED.
DR EMBL; U93036; AAB5620.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR001451; Hexapep_transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERSSES; UNKNOWN_1.
FT NON_TER 1 1
SQ SEQUENCE 602 AA; 51807 MW; 53BSB9A71EF04807 CRC64;

Query Match 59.2%; Score 296.5; DB 2; Length 602;
Best Local Similarity 66.3%; Pred. No. 2.2e-13;
Matches 67; Conservative 0; Mismatches 1; Indels 33; Gaps 1;

OY 1 VAAAKSAKVAKAQOLRAAAGIGAGIPGLGVGVPGIGVAGVPGIGVAGVPGFGAG 60
DB 531 VAAAKSAKVAKAQOLRAAAGIGAGIPGLGVGVPGIGVAGVPGIGVAGVPGFGA- 589
```

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OY 61 ADEGVRSLSPELREBDPSSSCHLPSTPSSPRVPGALAAK 101
DB 590 -----VPGALAAK 598

RESULT 13
ID 028099 PRELIMINARY; PRT; 650 AA.
AC 028099;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-2003 (TrEMBLrel. 24, Last annotation update)
DE Elastin-cBEL1; NCBI gi: 163003 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=85280426; PubMed=2992576;
RA Cicilia G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
RA Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
RT "Structure of the 3' portion of the bovine elastin gene."
RL Biochemistry 24:3075-3080(1985).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=88028442; PubMed=3665402;
RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Cicilia G., Yoon K., Rosenbloom J.;
RT "Sequence variation of bovine elastin mRNA due to alternative
RT splicing."
RL Coll. Relat. Res. 7:235-247(1987).
DR EMBL; M19372; AAA30499.1; -
DR EMBL; M1422; AAA30499.1; JOINED.
DR EMBL; M19366; AAA30499.1; JOINED.
DR EMBL; M19368; AAA30499.1; JOINED.
DR EMBL; M19369; AAA30499.1; JOINED.
DR EMBL; M19370; AAA30499.1; JOINED.
DR EMBL; M19371; AAA30499.1; JOINED.
DR EMBL; M22771; AAA30499.1; JOINED.
DR EMBL; M22772; AAA30499.1; JOINED.
DR EMBL; M22773; AAA30499.1; JOINED.
DR EMBL; M22774; AAA30499.1; JOINED.
DR EMBL; M22775; AAA30499.1; JOINED.
DR EMBL; M22988; AAA30499.1; JOINED.
DR EMBL; M23010; AAA30499.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
FT NON_TER 1 1
SQ SEQUENCE 650 AA; 55373 MW; CD21ABB3B9076AD7 CRC64;

Query Match 54.8%; Score 274.5; DB 2; Length 650;
Best Local Similarity 60.4%; Pred. No. 8.5e-12;
Matches 61; Conservative 1; Mismatches 6; Indels 33; Gaps 1;

OY 1 VAAAKSAKVAKAQOLRAAAGIGAGIPGLGVGVPGIGVAGVPGIGVAGVPGFGAG 60
DB 450 VAAAKSAKVAKAQOLRAAAGIGAGIPGLGVGVPGIGVAGVPGIGVAGVPGFGA- 508

OY 61 ADEGVRSLSPELREBDPSSSCHLPSTPSSPRVPGALAAK 101
DB 509 -----VPGTALAAK 517

RESULT 14
ID 028096 PRELIMINARY; PRT; 666 AA.
AC 028096;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
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DT 01-NOV-1996 (T-EMBLrel. 01, last sequence update)  
DT 01-JUN-2003 (T-EMBLrel. 24, last annotation update)  
DE Elastin-CBER3; NCBI gi: 163005 (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
NCBI\_TaxID=9913;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85280426; PubMed=2992576;  
RA Cicilia G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,  
RT Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;  
RL "Structure of the 3' portion of the bovine elastin gene."; Biochemistry 24:3075-3080(1985).  
RN (2)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88028442; PubMed=3665402;  
RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,  
RT Rosenbloom J.C., Cicilia G., Yoon K., Rosenbloom J.;  
RL "Sequence variation of bovine elastin mRNA due to alternative splicing."; Relat. Res. 7:235-247(1987).  
RT Coll. Relat. Res. 7:235-247(1987).  
DR EMBL; M19372; AAA30501.1; -.  
DR EMBL; M14422; AAA30501.1; JOINED.  
DR EMBL; M19366; AAA30501.1; JOINED.  
DR EMBL; M19366; AAA30501.1; JOINED.  
DR EMBL; M19368; AAA30501.1; JOINED.  
DR EMBL; M19368; AAA30501.1; JOINED.  
DR EMBL; M19370; AAA30501.1; JOINED.  
DR EMBL; M19370; AAA30501.1; JOINED.  
DR EMBL; M19371; AAA30501.1; JOINED.  
DR EMBL; M22771; AAA30501.1; JOINED.  
DR EMBL; M22771; AAA30501.1; JOINED.  
DR EMBL; M22772; AAA30501.1; JOINED.  
DR EMBL; M22773; AAA30501.1; JOINED.  
DR EMBL; M22775; AAA30501.1; JOINED.  
DR EMBL; M22775; AAA30501.1; JOINED.  
DR EMBL; M22988; AAA30501.1; JOINED.  
GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.  
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.  
DR InterPro; IPR003979; Tropoelastin.  
DR PRINTS; PR01500; TROPELASTIN.  
FT NON\_TER 1 1  
SQ SEQUENCE 666 AA; 56435 MW; BCB5E62632BE1B71 CRC64;  
Query Match 54.8%; Score 274.5; DB 2; Length 666;  
Best Local Similarity 60.4%; Pred. No. 8.6e-12;  
Matches 61; Conservative 1; Mismatches 6; Indels 33; Gaps 1;  
QY 1 VAAASAKVAAKQLRRAAGAGTGTGAGVGVGAGVPGTGTGAGVPGFGAG 60  
DB 458 VPAASAKVAAKQLRRAAGAGTGTGAGVGVGAGVPGTGTGAGVPGFGA- 516  
QY 61 ADEGVRRLSPBLREGDPSSQHLPTSPSPRVPGALAAK 101  
DB 517 -----VPGTILAAK 525  
RESULT 15  
Q28098 PRELIMINARY; PRT; 707 AA.  
AC Q28098; 01-NOV-1996 (T-EMBLrel. 01, Created)  
DT 01-NOV-1996 (T-EMBLrel. 01, last sequence update)  
DT 01-JUN-2003 (T-EMBLrel. 24, last annotation update)  
DE Elastin; NCBI gi: 163002 (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
NCBI\_TaxID=9913;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85280426; PubMed=2992576;

RA Cicilia G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,  
RA Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;  
RT "Structure of the 3' portion of the bovine elastin gene."; Biochemistry 24:3075-3080(1985).  
RN (2)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88028442; PubMed=3665402;  
RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,  
RT Rosenbloom J.C., Cicilia G., Yoon K., Rosenbloom J.;  
RL "Sequence variation of bovine elastin mRNA due to alternative splicing."; Relat. Res. 7:235-247(1987).  
RT Coll. Relat. Res. 7:235-247(1987).  
DR EMBL; M19372; AAA30498.1; -.  
DR EMBL; M14422; AAA30498.1; JOINED.  
DR EMBL; M19366; AAA30498.1; JOINED.  
DR EMBL; M19366; AAA30498.1; JOINED.  
DR EMBL; M19368; AAA30498.1; JOINED.  
DR EMBL; M19368; AAA30498.1; JOINED.  
DR EMBL; M19370; AAA30498.1; JOINED.  
DR EMBL; M19370; AAA30498.1; JOINED.  
DR EMBL; M19371; AAA30498.1; JOINED.  
DR EMBL; M22771; AAA30498.1; JOINED.  
DR EMBL; M22772; AAA30498.1; JOINED.  
DR EMBL; M22773; AAA30498.1; JOINED.  
DR EMBL; M22774; AAA30498.1; JOINED.  
DR EMBL; M22775; AAA30498.1; JOINED.  
DR EMBL; M22988; AAA30498.1; JOINED.  
GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.  
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.  
DR InterPro; IPR003979; Tropoelastin.  
DR PRINTS; PR01500; TROPELASTIN.  
FT NON\_TER 1 1  
SQ SEQUENCE 707 AA; 60346 MW; FDP559BAB34CE33 CRC64;  
Query Match 54.8%; Score 274.5; DB 2; Length 707;  
Best Local Similarity 60.4%; Pred. No. 9.1e-12;  
Matches 61; Conservative 1; Mismatches 6; Indels 33; Gaps 1;  
QY 1 VAAASAKVAAKQLRRAAGAGTGTGAGVGVGAGVPGTGTGAGVPGFGAG 60  
DB 484 VPAASAKVAAKQLRRAAGAGTGTGAGVGVGAGVPGTGTGAGVPGFGA- 542  
QY 61 ADEGVRRLSPBLREGDPSSQHLPTSPSPRVPGALAAK 101  
DB 543 -----VPGTILAAK 551  
Search completed: August 10, 2005, 07:37:42  
Job time : 114.06 secs

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